

OM nucleic - nucleic search, using sw model
Run on: October 21, 2003, 08:57:52 ; Search time 4611.42 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-1
Perfect score: 1803
Sequence: 1 gctacccccccacgcac.....cctaagcataggctttccag 1803

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba:*
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- 3: gb_in:*
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- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being print ,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1316.6	73.0	1323	10	AY246699	AY246699 Mus muscu
6	1187	65.8	1323	10	AY208915	AY208915 Rattus no
7	1064.8	59.1	1977	9	AF293357	AF293357 Homo sapi
8	1051	58.3	3742	6	AX210037	AX210037 Sequence
9	1016	56.4	3455	9	AF121259	AF121259 Homo sapi
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13	928.4	51.5	5857	9	AB033114	AB033114 Homo sapi
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15	924.4	51.3	3315	9	AK024357	AK024357 Homo sapi
16	865.4	48.0	1758	6	AX209989	AX209989 Sequence
17	865.4	48.0	3654	6	AX209987	AX209987 Sequence
18	865.4	48.0	3813	6	AX210064	AX210064 Sequence
19	863.8	47.9	1458	6	AX209991	AX209991 Sequence
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33	239.8	13.3	2850	6	AX210056	AX210056 Sequence

34 239.8 13.3 171075 2 AC026842 Homo sapi
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36 237.8 13.2 4021 9 AB018317 Homo sapi
c 37 236.6 13.1 100000 9 AB020864 Homo sapi
38 236.6 13.1 131299 9 AF165145 Homo sapi
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41 213.2 11.8 4442 10 AB093263 Mus muscu
42 205.2 11.4 1003 5 AF176665 Xenopus l
c 43 195 10.8 595 11 BV035724 Mus muscu
44 162 9.0 700 6 AX210048 Homo sapi
45 160.4 8.9 186901 2 AF267167 Homo sapi

ALIGNMENTS

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LOCUS Mus musculus angiotensin II AT2 receptor-interacting protein mRNA,
DEFINITION complete cds.
ACCESSION AF173380
VERSION AF173380.1 GI:5733813
KEYWORDS Mus musculus (house mouse)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1803)
REFERENCE Elbaz,N., Strosberg,A.D. and Nahmias,C.
AUTHORS Molecular characterization of ATIP, a novel angiotensin II type 2
TITLE receptor-interacting protein
JOURNAL Unpublished
2 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1999) Institut Cochin de Genetique Moleculaire,
CNRS UPR415, 22, rue Mechain, Paris 75014, France
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/note="ATIP"
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/protein_id="AAD49746.1"
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Job time : 4620.42 secs

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QY 1141 GAGAGCTGCACCGAGAGCAATGAAGCTAATGAGATGGAAGCTGGTGACATTAAC 1200
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Db 1501 CGGCTTCTGAAGGAGAGACTCTCTGAGGAGACTGAGGTGCGCTTCTGAGGACTGACC 1560
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OM nucleic - nucleic search, using sw model
Run on: October 21, 2003, 08:56:18 ; Search time 346.674 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-1
Perfect score: 1803
Sequence: 1 gctacccccccacgac.....cctaagcataggtttccag 1803

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : N_Geneseq_19Jun03:*
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 - 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
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 - 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
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 - 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
 - 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
 - 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
 - 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
 - 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
 - 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
 - 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
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 - 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
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 - 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
 - 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
 - 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
 - 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
 - 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
 - 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
 - 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
 - 25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1803	100.0	1803	21	AAZ99088
2	1323	73.4	1323	21	AAZ99089
3	1051	58.3	3742	21	AAZ99091
4	1051	58.3	3742	22	AAH74362
5	1003.6	55.7	1615	24	AAZ99095
6	941.8	52.2	1308	21	AAZ99092
7	925.2	51.3	5799	22	AAH74383
8	924.4	51.3	3315	22	AAH18632
9	924.2	51.3	4937	25	ABX63076
10	923.6	51.2	5961	22	AAH74385
11	886.6	49.2	1369	22	AAH74322
12	868.4	48.2	3807	25	ABX10230
13	865.4	48.0	1758	22	AAH74324
14	865.4	48.0	3654	22	AAH74323
15	863.8	47.9	1458	22	AAH74325
16	863.8	47.8	1191	22	AAH74326
17	844.8	35.8	910	24	ABSS1467
18	540.8	30.0	775	22	AAH74327
19	521.4	28.9	3287	21	AAF22392
20	515.8	28.6	830	22	AAH07946
21	354	19.6	354	21	AAZ99090
22	342.2	19.0	656	22	AAZ26578
23	342.2	19.0	656	25	ABX73919
24	337	18.7	791	25	AAZ53121
25	304.6	16.9	481	22	AAZ26163
26	304.6	16.9	481	25	ABX73504
27	239.8	13.3	2850	22	AAH74380
28	237.8	13.2	4184	25	ABX71114
29	233.8	13.0	2333	22	AAH74361
30	212.8	11.8	435	25	ABX53761
31	174.8	9.7	242	25	ABX74609
32	162	9.0	700	22	AAH74372
33	159	8.8	215	22	AAH74353
34	143	7.9	900	22	AAH74371
35	143	7.9	2672	24	ABK09997
36	142.6	7.9	413	22	AAH74352
37	138.6	7.7	367	22	AAH74329
38	130	7.2	338	21	AAA41587
39	128	7.1	562	23	ABV48083
40	106.6	5.9	700	22	AAH74374
41	104.2	5.8	133	24	ABV88907
42	102.8	5.7	203	22	AAH74355
43	93.4	5.2	600	22	AAH74378
44	92.8	5.1	120	22	AAH74363
45	91.8	5.1	1370	22	AAZ06852

ALIGNMENTS

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCTACCCGCCCCCAGCAGCACCCCCCAATCTGGGTGGCTGGCATTAGCATGTAGGCTTGT	60
DB	1	GCTACCCGCCCCCAGCAGCACCCCCCAATCTGGGTGGCTGGCATTAGCATGTAGGCTTGT	60
QY	61	TTTTCTCTGGCTGTATCTTTGGGCTGGAAAGAACCCCGAGTTGCCAAGACACAGTAT	120
DB	61	TTTTCTCTGGCTGTATCTTTGGGCTGGAAAGAACCCCGAGTTGCCAAGACACAGTAT	120
QY	121	TGATGGTCCCTGGAAAAGCTGCTTCCCTGGGAAGTTCTCCACTGGCTTCGAAGACAT	180
DB	121	TGATGGTCCCTGGAAAAGCTGCTTCCCTGGGAAGTTCTCCACTGGCTTCGAAGACAT	180
QY	181	CTGTGTCTCCCAANTCTCTTATCCACATCCAGCTCCGGCTAACGCCAAGACAT	240
DB	181	CTGTGTCTCCCAANTCTCTTATCCACATCCAGCTCCGGCTAACGCCAAGACAT	240
QY	241	CTTCGAACCTCCGGCTTCTTTCCGGGGCTCAGGAAAAACACTGTCTATTTCCACAGAT	300
DB	241	CTTCGAACCTCCGGCTTCTTTCCGGGGCTCAGGAAAAACACTGTCTATTTCCACAGAT	300
QY	301	GAAGGGGAGGAGAGAGATCCCAAGAGCTGTGCATCCAGACCCAGACAGCTCCAGAT	360
DB	301	GAAGGGGAGGAGAGAGATCCCAAGAGCTGTGCATCCAGACCCAGACAGCTCCAGAT	360
QY	361	GTGTGTCTCCGAGAGACGCTTGAGTTGGGCCCAATACAGACAAATGTGAAGCCAA	420
DB	361	GTGTGTCTCCGAGAGACGCTTGAGTTGGGCCCAATACAGACAAATGTGAAGCCAA	420
QY	421	AGTGGATTCTCTGACACCTCAGGAGCTTCTTCCCGTGGTAAACAACAAGTGAAGCG	480
DB	421	AGTGGATTCTCTGACACCTCAGGAGCTTCTTCCCGTGGTAAACAACAAGTGAAGCG	480
QY	481	CTGACAGTTGTATCCAGCACTCTCTGTGAGCGGGAGGAGGAGCTGAAGCAGACAAA	540
DB	481	CTGACAGTTGTATCCAGCACTCTCTGTGAGCGGGAGGAGGAGCTGAAGCAGACAAA	540
QY	541	ACCTCTCTCAAGAACTTGTGAGGCTCCGGGAGAGCTAGTTGCTTCAAGCGCTGT	600
DB	541	ACCTCTCTCAAGAACTTGTGAGGCTCCGGGAGAGCTAGTTGCTTCAAGCGCTGT	600
QY	601	GAGAGCTAGAAAAGGCTAGGGCTGACTTACAGACAGCGTATCAAGAATTTGTCCAGAAA	660
DB	601	GAGAGCTAGAAAAGGCTAGGGCTGACTTACAGACAGCGTATCAAGAATTTGTCCAGAAA	660
QY	661	CTAAACGACGAGATCAGACAGACCGGAGGAGCTGGAGACCGGCTGAAGGACTTATAC	720
DB	661	CTAAACGACGAGATCAGACAGACCGGAGGAGCTGGAGACCGGCTGAAGGACTTATAC	720
QY	721	ACCGCAGAGTGTGAGAGGCTTCAGAGCATTTACATTGAGGAGGAGAGAAAATATAAACT	780
DB	721	ACCGCAGAGTGTGAGAGGCTTCAGAGCATTTACATTGAGGAGGAGAGAAAATATAAACT	780
QY	781	CACTCCAGAGAGGTTTGACACTTAACGGCGGCCCATGAGACCATTAAGCTTGAGTT	840
DB	781	CACTCCAGAGAGGTTTGACACTTAACGGCGGCCCATGAGACCATTAAGCTTGAGTT	840

RESULT 1
AAZ99088 standard; cDNA; 1803 BP.
XX ID AAZ99088 standard; cDNA; 1803 BP.
XX AC AAZ99088;
XX DT 21-JUN-2000 (first entry)
XX DE Mouse ATIP gene.
XX KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
XX KW two-hybrid screen; signal transduction.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX CDS 178
XX FT /*tag= a
XX FT /product= "ATIP"
XX FT /note= "angiotensin II (AT2) receptor interactive
XX FT protein"
XX PN FR2782084-A1.
XX PD 11-FEB-2000.
XX PF 04-AUG-1998; 98FR-0009997.
XX PR 04-AUG-1998; 98FR-0009997.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Elbaz N, Nahmias C, Strosberg AD;
XX DR WPI; 2000-248410/22.
XX DR P-PSDB; AAY83777.
XX PT Nucleic acids coding for angiotensin II receptor AT2 interacting
XX PS proteins useful in screening assays for receptor-protein interaction -
XX PS Claim 1; Fig 3; 63pp; French.
XX CC This sequence represents the cDNA encoding a mouse angiotensin II (AT2)
XX CC receptor interactive protein (ATIP). The gene was isolated from a
XX CC two-hybrid screen using the C-terminal fragment of the mouse AT2
XX CC receptor as the "bait" (AAY83781). The "target" is a mouse foetal cDNA
XX CC library. Cells transformed with vectors containing the cDNA, or
XX CC immobilized proteins encoded by it, can be used to screen for substances
XX CC that modulate ATIP-AT2 interaction or substances that interact with
XX CC ATIP, especially using yeast two- or three-hybrid techniques. Such
XX CC substances may be useful for treating disorders associated with anomalous
XX CC AT2 receptor signal transduction.
XX SQ Sequence 1803 BP; 539 A; 464 C; 440 G; 360 T; 0 other;
Query Match 100.0%; Score 1803; DB 21; Length 1803;

Db 761 CAAGTGAAGAGAGATTTCACAACTTAAAGCGCGCCCATGAGACCCTTAAGCTTGAGATT 840

QY 841 GAGCTAGCCCTCGAGAAAGCTGGAAATGCTGAAGAGACCTATGAAGCCTCCCTTCA 900

Db 841 GAGCTAGCCCTCGAGAAAGCTGGAAATGCTGAAGAGACCTATGAAGCCTCCCTTCA 900

QY 901 GAAATCAAGAGAGCCATGAGATGGAGAGAAAGTCACTGGAGATCTGCTTAATGAGAAG 960

Db 901 GAAATCAAGAGAGCCATGAGATGGAGAGAAAGTCACTGGAGATCTGCTTAATGAGAAG 960

QY 961 CAGGAATCCCTGGAGAAACAAATCAATGATCTGAAGATGAAAACGATGCTTTAAACGAA 1020

Db 961 CAGGAATCCCTGGAGAAACAAATCAATGATCTGAAGATGAAAACGATGCTTTAAACGAA 1020

QY 1021 AGGTTGAATCAGAGAGAGCAAAACAACTGTCAAGAGAGAGCGCAATTCAAAACCTT 1080

Db 1021 AGGTTGAATCAGAGAGAGCAAAACAACTGTCAAGAGAGAGCGCAATTCAAAACCTT 1080

QY 1081 CAGGTCATGTATCTGGAGCAAGACTAGAAAGCCTGAAGCTGTGTAGAGATCAAGAAAT 1140

Db 1081 CAGGTCATGTATCTGGAGCAAGACTAGAAAGCCTGAAGCTGTGTAGAGATCAAGAAAT 1140

QY 1141 GAGAACTGCACCGAGAGGACATGAAGCTAATGAAGTGGAAAGCTGGTGGACATAC 1200

Db 1141 GAGAACTGCACCGAGAGGACATGAAGCTAATGAAGTGGAAAGCTGGTGGACATAC 1200

QY 1201 ACAGCATTTGGTTGAAGCTGAAGCAATCCAGAGAGAAACGAGAGTTAAAGCTCGC 1260

Db 1201 ACAGCATTTGGTTGAAGCTGAAGCAATCCAGAGAGAAACGAGAGTTAAAGCTCGC 1260

QY 1261 ATGAGCAAAACATGGCAATTTCAAGGCAACTTTCACCGAGAGCGCGCTGGAAGAG 1320

Db 1261 ATGAGCAAAACATGGCAATTTCAAGGCAACTTTCACCGAGAGCGCGCTGGAAGAG 1320

QY 1321 TCCCTTGAGAGAGGTCAAGAGTCAAGAGAGACTGTCCATGGAGAACGAGGAACTTCTG 1380

Db 1321 TCCCTTGAGAGAGGTCAAGAGTCAAGAGAGACTGTCCATGGAGAACGAGGAACTTCTG 1380

QY 1381 TGGAACTGCACAGAGGAGACTGTGCAGGCCCCAAGAGATCCCCCACTCTCTCGGCCATC 1440

Db 1381 TGGAACTGCACAGAGGAGACTGTGCAGGCCCCAAGAGATCCCCCACTCTCTCGGCCATC 1440

QY 1441 CTTTCCAGTCCCCCAGGAATTCGTGTTCTCTGAAGGCACTGAGTGGCTTCTGCAGGACTGACC 1500

Db 1441 CTTTCCAGTCCCCCAGGAATTCGTGTTCTCTGAAGGCACTGAGTGGCTTCTGCAGGACTGACC 1500

QY 1501 CGGCTTCTGAAGCAGAGAGACTCTCTGAAGGCACTGAGTGGCTTCTGCAGGACTGACC 1560

Db 1501 CGGCTTCTGAAGCAGAGAGACTCTCTGAAGGCACTGAGTGGCTTCTGCAGGACTGACC 1560

QY 1561 CTCTCATGGGAATCGAGTTGCTGGTTAGCTCTCTGGAATATCCCCAGGAATTCGGGAG 1620

Db 1561 CTCTCATGGGAATCGAGTTGCTGGTTAGCTCTCTGGAATATCCCCAGGAATTCGGGAG 1620

QY 1621 AGCAGCGCGCAACCTATCAGCTAGTACGAATAGAGAGCTCCCAATAGAGACTTTTAAC 1680

Db 1621 AGCAGCGCGCAACCTATCAGCTAGTACGAATAGAGAGCTCCCAATAGAGACTTTTAAC 1680

QY 1681 TTGGTCCAAAAGCCTCTCCAAAAACAGATTTGGAACTGAAGTGGACATAGTTGCACAA 1740

Db 1681 TTGGTCCAAAAGCCTCTCCAAAACAGATTTGGAACTGAAGTGGACATAGTTGCACAA 1740

QY 1741 AGCACTTAGGAGAGGAGGAAACCTTGTCTTTGGCTTCCCTCACCTAAGCCTAGGCTTTC 1800

Db 1741 AGCACTTAGGAGAGGAGGAAACCTTGTCTTTGGCTTCCCTCACCTAAGCCTAGGCTTTC 1800

QY 1801 CAG 1803

Db 1801 CAG 1803

Search completed: October 21, 2003, 11:10:58
Job time : 353.674 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 368.905 Seconds
 (without alignments)
 13107.136 Million cell updates/sec

Title: US-09-762-194-1
 Perfect score: 1803
 Sequence: 1 gctacccccccacgcac.....cctaagcataggtttccag 1803

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues 3584790

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq**	4937	13	US-10-044-090-76	Sequence 71, Appl
2:	/cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq**	910	14	US-10-043-487-47	Sequence 47, Appl
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq**	656	10	US-09-764-864-757	Sequence 757, App
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq**	342.2	19.0	US-09-764-864-342	Sequence 343, App
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq**	304.6	16.9	US-09-918-995-5132	Sequence 513, App
6:	/cgn2_6/ptodata/1/pubpna/FCIUS_PUBCOMB.seq**	271.4	15.1	US-09-983-965-3690	Sequence 369, App
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq**	212.8	11.8	US-09-918-995-5569	Sequence 5569, App
8:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq**	166.2	9.2	US-09-918-995-12481	Sequence 12481, A
9:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq**	156.8	8.7	US-10-027-632-85144	Sequence 85144, A
10:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq**	131.8	7.3	US-09-918-995-11578	Sequence 11578, A
11:	/cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq**	104.2	5.8	US-09-998-598-2218	Sequence 2218, App
12:	/cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq**	91.4	5.1	US-09-925-302-132	Sequence 132, App
13:	/cgn2_6/ptodata/1/pubpna/US09F_PUBCOMB.seq**	67	3.7	US-10-294-804-1	Sequence 1, Appl
14:	/cgn2_6/ptodata/1/pubpna/US09G_PUBCOMB.seq**	55.2	3.1	US-10-029-386-22859	Sequence 22859, A
15:	/cgn2_6/ptodata/1/pubpna/US09H_PUBCOMB.seq**	54.4	3.0	US-10-029-386-19974	Sequence 19974, A
16:	/cgn2_6/ptodata/1/pubpna/US09I_PUBCOMB.seq**	54.4	3.0	US-10-029-386-6243	Sequence 6243, App
17:	/cgn2_6/ptodata/1/pubpna/US09J_PUBCOMB.seq**	54.2	3.0	US-10-004-113-7	Sequence 7, Appl
18:	/cgn2_6/ptodata/1/pubpna/US09K_PUBCOMB.seq**	51.8	2.9	US-10-101-487-74	Sequence 74, Appl
19:	/cgn2_6/ptodata/1/pubpna/US09L_PUBCOMB.seq**	51.8	2.9	US-10-101-487-76	Sequence 76, Appl
20:	/cgn2_6/ptodata/1/pubpna/US09M_PUBCOMB.seq**	50.2	2.8	US-09-864-761-20733	Sequence 20733, A
21:	/cgn2_6/ptodata/1/pubpna/US09N_PUBCOMB.seq**	50.2	2.8	US-09-864-761-3972	Sequence 3972, App
22:	/cgn2_6/ptodata/1/pubpna/US09O_PUBCOMB.seq**	49.8	2.8	US-09-764-853-887	Sequence 887, App
23:	/cgn2_6/ptodata/1/pubpna/US09P_PUBCOMB.seq**	49.8	2.8	US-09-764-853-937	Sequence 937, App
24:	/cgn2_6/ptodata/1/pubpna/US09Q_PUBCOMB.seq**	49.8	2.8	US-10-091-438-250	Sequence 250, App
25:	/cgn2_6/ptodata/1/pubpna/US09R_PUBCOMB.seq**	49.8	2.8	US-09-764-853-886	Sequence 886, App
26:	/cgn2_6/ptodata/1/pubpna/US09S_PUBCOMB.seq**	49.8	2.8	US-09-764-853-933	Sequence 933, App
27:	/cgn2_6/ptodata/1/pubpna/US09T_PUBCOMB.seq**	49.8	2.8	US-10-091-438-246	Sequence 246, App
28:	/cgn2_6/ptodata/1/pubpna/US09U_PUBCOMB.seq**	49.8	2.8	US-10-091-438-255	Sequence 255, App
29:	/cgn2_6/ptodata/1/pubpna/US09V_PUBCOMB.seq**	49.8	2.8	US-09-864-761-18355	Sequence 18355, A
30:	/cgn2_6/ptodata/1/pubpna/US09W_PUBCOMB.seq**	49.4	2.7	US-09-864-761-6203	Sequence 6203, App
31:	/cgn2_6/ptodata/1/pubpna/US09X_PUBCOMB.seq**	49.4	2.7	US-09-864-761-22817	Sequence 22817, A
32:	/cgn2_6/ptodata/1/pubpna/US09Y_PUBCOMB.seq**	48.2	2.7	US-09-738-973-157	Sequence 157, App
33:	/cgn2_6/ptodata/1/pubpna/US09Z_PUBCOMB.seq**	48.2	2.7	US-09-854-133-157	Sequence 157, App
34:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq**	48.2	2.7	US-10-144-649A-157	Sequence 157, App
35:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq**	48.2	2.7	US-09-764-868-12	Sequence 12, Appl
36:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq**	48.2	2.7	US-10-233-045-35	Sequence 35, Appl
37:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq**	47	2.6	US-10-001-870-68	Sequence 68, Appl
38:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq**	46.6	2.6	US-10-029-386-12333	Sequence 12333, A
39:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq**	46.6	2.6	US-10-029-386-26033	Sequence 26033, A
40:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq**	46.6	2.6	US-09-938-842A-85	Sequence 85, Appl
41:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq**	46.2	2.6	US-09-864-761-17529	Sequence 17529, A
42:	/cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq**	46.2	2.6	US-10-311-455-1670	Sequence 1670, App
43:	/cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq**	45.8	2.5	US-09-864-761-18684	Sequence 18684, A
44:	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq**	45.6	2.5	US-09-771-208-20	Sequence 20, Appl
45:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq**				

Search completed: October 22, 2003, 03:34:38
 Job time : 371.905 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description

OM nucleic - nucleic search, using sw model
Run on: October 21, 2003, 09:08:27 ; Search time 2842.6 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-1
Perfect score: 1803
Sequence: 1 gctacccccccacgcac.....cctaagcataggctttccag 1803

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_fod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1750.2	97.1	2477	11	AK030510	AK030510 Mus muscu
2	1732.6	96.1	3963	11	AK031693	AK031693 Mus muscu
3	1249.6	69.3	3237	11	AK035576	AK035576 Mus muscu
4	896.6	49.7	950	13	BQ921402	BQ921402 AGENCOURT
5	845.8	46.9	920	13	BQ523654	BQ523654 AGENCOURT
6	618.4	34.3	712	10	BB567855	BB567855 BB567855
7	614.2	34.1	1005	13	BQ070423	BQ070423 AGENCOURT
8	604.4	33.5	657	10	BB628131	BB628131 BB628131
9	598	33.2	623	10	BF577785	BF577785 602092084
10	595.2	33.0	748	10	BF141309	BF141309 60179830
11	593.8	32.9	907	13	BQ593171	BQ593171 AGENCOURT
12	592	32.8	624	12	BM951991	BM951991 UI-M-EHO-
13	583	32.3	937	10	BF607509	BF607509 MY_00045
14	579.6	32.1	782	13	BQ702398	BQ702398 UI-M-FIO-
15	567.4	31.5	734	14	CB316595	CB316595 AGENCOURT
16	564.6	31.3	600	13	BQ921755	BQ921755 6093-85 M
17	562.8	31.2	742	13	BQ204579	BQ204579 UI-R-DZ1-
18	552	30.6	553	12	BG800655	BG800655 0051-47 M
19	538.4	29.9	541	4	BX512030	BX512030 NZPD Mus
20	536	29.7	605	12	BI654474	BI654474 603281030
21	535.4	29.7	648	10	BB656106	BB656106 BB656106
22	529.8	29.4	639	12	BM946483	BM946483 UI-M-EMO-
23	523.4	29.0	782	9	AU141757	AU141757 AU141757
24	516	28.6	1346	11	BQ007328	BQ007328 Homo sapi
25	515.8	28.6	830	9	AU138373	AU138373 AU138373
26	513.8	28.5	517	10	BB652532	BB652532 UI-M-AMO-
27	510.6	28.3	530	13	BQ830956	BQ830956 LL61n1027
28	508.6	28.2	710	14	CB723104	CB723104 UI-M-GHO-
29	508.4	28.2	560	14	CD565243	CD565243 B0491H11-
30	504.2	28.0	711	14	BY739988	BY739988 BY739988
31	502.9	27.9	509	12	BI319660	BI319660 Iel4a05.y
32	498.4	27.6	500	9	AA880300	AA880300 vx39f05.r
33	494	27.4	629	10	BB662397	BB662397 BB662397
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35	485.4	26.9	634	14	BY740600	BY740600 BY740600
36	485	26.9	634	14	BY740600	BY740600 BY740600
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38	478.8	26.6	728	13	BQ745000	BQ745000 UI-M-EHO-
39	477.8	26.5	630	10	BB617931	BB617931 BB617931
40	477.8	26.5	664	14	BY726879	BY726879 BY726879
41	467.4	25.9	469	14	CA531568	CA531568 C03-1B05-
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43	463.4	25.7	474	9	AA980079	AA980079 ua28c.1.r
44	459.8	25.3	732	12	BM951385	BM951385 UI-M-EHO-
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 3383.75 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-3

Perfect score: 1323

Sequence: 1 atgtgtgtgtctcccaatt.....ccagcatctcaccagatga 1323

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: gb_in:*
- 4: gb_om:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	1203.4	91.0	5219	10	BC042206	BC042206 Mus musculus
5	1193.8	90.2	3629	10	BC043321	BC043321 Mus musculus
6	1187	89.7	1323	10	AY208915	AY208915 Rattus norvegicus
7	956.2	72.3	1977	9	AF293357	AF293357 Homo sapiens
8	956.2	72.3	3455	9	AF121259	AF121259 Homo sapiens
9	953	72.0	1615	6	AX301208	AX301208 Sequence
10	941.8	71.2	3742	6	AX210037	AX210037 Sequence
11	865.4	65.4	1758	6	AX209989	AX209989 Sequence
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13	865.4	65.4	3813	6	AX210064	AX210064 Sequence
14	865.4	65.4	5799	6	AX210061	AX210061 Sequence
15	865.4	65.4	5857	9	AB033114	AB033114 Homo sapiens
16	864.6	65.4	3315	6	BD160624	BD160624 Primer for
17	864.6	65.4	3315	9	AK024357	AK024357 Homo sapiens
18	863.8	65.3	1458	6	AX209591	AX209591 Sequence
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20	861.8	65.1	1191	6	AX209993	AX209993 Sequence
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22	570.2	43.1	2895	9	BC033842	BC033842 Homo sapiens
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25	325.6	24.6	2548	9	AK000172	AK000172 Homo sapiens
26	315	23.6	1229	10	BC030860	BC030860 Mus musculus
27	250.6	18.9	729	9	H0267D11	H0267D11 Homo sapiens
28	250.6	18.9	2235	9	AK093875	AK093875 Homo sapiens
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31	216.2	16.3	194355	2	AC116511	AC116511 Mus musculus
32	212.2	16.0	4445	2	AB093263	AB093263 Homo sapiens
33	205.2	15.5	1003	5	AF176665	AF176665 Xenopus laevis

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Mus musculus angiotensin II AT2 receptor-interacting protein mRNA, complete cds.
ACCESSION AF173380
VERSION AF173380.1 GI:5733813
KEYWORDS Mus musculus (house mouse)
SOURCE Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Molecular characterization of Arip, a novel angiotensin II type 2 receptor-interacting protein
JOURNAL Unpublished
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1999) Institut Cochin de Genetique Moleculaire, CNRS UPR415, 22, rue Mechain, Paris 75014, France
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BASE COUNT 539 a 464 c 440 g 360 t
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Query Match 100.0%; Score 1323; DB 10; Length 1803;
Best Local Similarity 100.0%; Pred. No. 0;
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DB 1498 TGA 1500

RESULT 2
AY246699
LOCUS AY246699 1323 bp mRNA linear ROD 10-APR-2003
DEFINITION Mus musculus MTSG1 mRNA, complete cds.
ACCESSION AY246699
VERSION AY246699.1 GI:29725653
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1323)
AUTHORS Seibold,S., Wanner,C. and Galle,J.
TITLE Cloning and characterization of MTS1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1323)
AUTHORS Seibold,S., Wanner,C. and Galle,J.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2003) Department of Medicine, University of
Wuerzburg, Josef Schneider Str 2, Wuerzburg 97060, Germany
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Search completed: October 21, 2003, 17:17:54
Job time : 3388.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:18 : Search time 254.382 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-3
Perfect score: 1323
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1323	100.0	1323	21	AAZ99089
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6	941.8	71.2	3742	22	AAH74362
7	865.4	65.4	1758	22	AAH74324
8	865.4	65.4	3654	22	AAH74323
9	865.4	65.4	3807	25	ABX10230
10	865.4	65.4	4937	25	ABX63076
11	864.6	65.4	3315	22	AAH19632
12	863.8	65.3	1369	22	AAH74322
13	863.8	65.3	1458	22	AAH74325
14	863.8	65.3	5799	22	AAH74383
15	862.2	65.2	5961	22	AAH74385
16	861.8	65.1	1191	22	AAH74326
17	644.8	48.7	910	24	ABSS1467
18	518	39.2	775	22	AAH74327
19	515.8	39.0	830	22	AAH07946
20	460	34.8	3287	21	AAF22392
21	354	26.8	354	21	AAZ99090
22	342.2	25.9	656	22	AS26578
23	342.2	25.9	656	25	ABX73919
24	337	25.5	791	25	AAD53121
25	304.6	23.0	481	22	AS26163
26	304.6	23.0	481	25	ABX73504
27	235.4	17.8	4184	25	ABX71114
28	212.8	16.1	435	25	ABX53761
29	176.8	13.4	2850	22	AAH74380
30	174.8	13.2	242	25	ABX74609
31	170.8	12.9	2333	22	AAH74361
32	162	12.2	700	22	AAH74372
33	159	12.0	215	22	AAH74353
34	130	9.8	338	21	AAH41587
35	128	9.7	562	23	ABV48083
36	106.6	8.1	700	22	AAH74374
37	104.2	7.9	133	24	ABV88907
38	102.8	7.8	203	22	AAH74355
39	94.2	7.1	900	22	AAH74371
40	94.2	7.1	2672	24	ABK09997
41	93.8	7.1	413	22	AAH74352
42	93.4	7.1	600	22	AAH74378
43	92.8	7.0	120	22	AAH74363
44	91.8	6.9	1370	22	AAD08852
45	91.8	6.9	2993	22	AAH18194

ALIGNMENTS

RESULT 1

AAZ99089
ID AAZ99089 standard; cDNA; 1323 BP.

XX	AC	AAZ99089;			
XX	DF	21-JUN-2000 (first entry)			
XX	DE	Mouse ATIP coding sequence.			
XX	KW	Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;			
XX	KW	two-hybrid screen; signal transduction; coding sequence.			
XX	OS	Mus sp.			
XX	FN	FR2782084-A1.			
XX	PD	11-FEB-2000.			
XX	PF	04-AUG-1998; 98FR-0009997.			
XX	PR	04-AUG-1998; 98FR-0009997.			
XX	PA	(CNRS) CNRS CENT NAT RECH SCI.			
XX	PI	Elbaz N, Nahmias C, Strosberg AD;			
XX	DR	WPI; 2000-248410/22.			
XX	DR	P-PSDB; AAY83777.			
XX	PT	Nucleic acids coding for angiotensin II receptor AT2 interacting			
XX	PT	proteins useful in screening assays for receptor-protein interaction -			
XX	PS	Claim 1; Page 30-31; 63pp; French.			
XX	CC	This sequence represents the open reading frame (ORF) of the cDNA			
XX	CC	encoding a mouse angiotensin II (AT2) receptor interactive protein			
CC	CC	(ATIP). The gene was isolated from a two-hybrid screen using the			
CC	CC	C-terminal fragment of the mouse AT2 receptor as the "bait" (AAY8378).			
CC	CC	The "target" is a mouse foetal cDNA library. Cells transformed with			
CC	CC	vectors containing the cDNA, or immobilized proteins encoded by it,			
CC	CC	can be used to screen for substances that modulate ATIP-AT2 interaction			
CC	CC	or substances that interact with ATIP, especially using yeast two-			
CC	CC	three-hybrid techniques. Such substances may be useful for treating			
CC	CC	disorders associated with anomalous AT2 receptor signal transduction			
SQ		Sequence 1323 BP; 425 A; 326 C; 325 G; 247 T; 0 other;			
Query Match 100.0%; Score 1323; DB 21; Length 1323;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGCTGTGTCTCCCAATTCTCTTATCCACCTCCAGTCCGCTAACCGCAAGGA	60		
DB	1	ATGCTGTGTCTCCCAATTCTCTTATCCACCTCCAGTCCGCTAACCGCAAGGA	60		

Db	901	CTCAGGTCATGATCTGGACGAAGAACTAGAAAGGCTGAAGGCTGTGTAGATCAAG	960
QY	961	AATGAGAAGCTGCACCAGCAGGACATGAAGCTAATGAAGATGGAAAAAGCTGGTGCAAT	1020
Db	961	AATGAGAAGCTGCACCAGCAGGACATGAAGCTAATGAAGATGGAAAAAGCTGGTGCAAT	1020
QY	1021	AACACAGCAATGGTTGACAGCTGAAGGATTCACGAGGAAAAACGAGAGTAAAAGCT	1080
Db	1021	AACACAGCAATGGTTGACAGCTGAAGGATTCACGAGGAAAAACGAGAGTAAAAGCT	1080
QY	1081	CGCATGGACAACACATGGCAATTTCAAGGCACCTTTCCACCGACGACGGCGCGCTGCAA	1140
Db	1081	CGCATGGACAACACATGGCAATTTCAAGGCACCTTTCCACCGACGACGGCGCGCTGCAA	1140
QY	1141	GAGTCCCTTGAGAGGAGTCAAAAGGTCACCAAGAGACTGTCCATGAGAGAACGAGGAAGCT	1200
Db	1141	GAGTCCCTTGAGAGGAGTCAAAAGGTCACCAAGAGACTGTCCATGAGAGAACGAGGAAGCT	1200
QY	1201	CTGTGGAAACTGCACAGGAGACCTGTGCAGGCCCAAGAGATCCCCCACTCCTCGGCT	1260
Db	1201	CTGTGGAAACTGCACAGGAGACCTGTGCAGGCCCAAGAGATCCCCCACTCCTCGGCT	1260
QY	1261	ATCCCTTTCCAGTCCCCCAGGAATTCGTGTCTTCATCCAGCCCCCAGATCTCACCCAG	1320
Db	1261	ATCCCTTTCCAGTCCCCCAGGAATTCGTGTCTTCATCCAGCCCCCAGATCTCACCCAG	1320
QY	1321	TGA 1323	
Db	1321	TGA 1323	
RESULT 2			
AAZ99088			
ID	AAZ99088 standard; cDNA; 1803 BP.		
XX	AAZ99088;		
XX			
DT	21-JUN-2000 (first entry)		
XX			
DE	Mouse ATIP gene.		
XX			
KW	Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;		
KW	two-hybrid screen; signal transduction.		
OS	Mus sp.		
FX	Key	Location/Qualifiers	
FT	CDS	178	
FT	FT	/*tag= a	
FT	FT	/product= "ATIP"	
FT	FT	/note= "angiotensin II (AT2) receptor interactive	
FT	FT	protein"	
XX	FR2782084-A1.	FN	
XX	PD	11-FEB-2000.	

XX 04-AUG-1998; 98FR-0009997.
PF 04-AUG-1998; 98FR-0009997.
PR 04-AUG-1998; 98FR-0009997.
XX (CNRS) CNRS CENT NAT RECH SCI.
PA Elbaz N, Nalmias C, Strosberg AD;
XX
XX WPI: 2000-248410/22.
DR P-PSDB; AY83777.
XX
XX Nucleic acids coding for angiotensin II receptor AT2 interacting
PT proteins useful in screening assays for receptor-protein interaction -
XX
XX Claim 1; Fig 3; 63pp; French.
XX
XX This sequence represents the cDNA encoding a mouse angiotensin II (AT2)
CC receptor interactive protein (ATIP). The gene was isolated from a
CC two-hybrid screen using the C-terminal fragment of the mouse AT2
CC receptor as the "bait" (AY83781). The "target" is a mouse foetal cDNA
CC library. Cells transformed with vectors containing the cDNA, or
CC immobilized proteins encoded by it, can be used to screen for substances
CC that modulate ATIP-AT2 interaction or substances that interact with
CC ATIP, especially using yeast two- or three-hybrid techniques. Such
CC substances may be useful for treating disorders associated with anomalous
CC AT2 receptor signal transduction.
XX
XX Sequence 1803 BP; 539 A; 464 C; 440 G; 360 T; 0 other;

Query Match 100.0%; Score 1323; DB 21; Length 1803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGTCCTCCAAATTCCTTATCCACCATCCAGCTCCGCTAACCGCAAGGA 60
DB 178 ATGCTGTTGTCCTCCAAATTCCTTATCCACCATCCAGCTCCGCTAACCGCAAGGA 237
QY 61 CTGCTTCGAAACCTCCGCTTCCTTCGGGGCTCAGGAAACACACTGTCAATTTCCACACA 120
DB 238 CTGCTTCGAAACCTCCGCTTCCTTCGGGGCTCAGGAAACACACTGTCAATTTCCACACA 297
QY 121 GTTGAAAGGGCAGCAGAGAAATCCACAGAGCTGTGCATCCAGACCCAGACAGCTCCA 180
DB 298 GTTGAAAGGGCAGCAGAGAAATCCACAGAGCTGTGCATCCAGACCCAGACAGCTCCA 357
QY 181 GATGTGCTGTCTCCGAGAGAACGCTTGAGTTGGCCCAATACAGACAAATGTGAAGC 240
DB 356 GATGTGCTGTCTCCGAGAGAACGCTTGAGTTGGCCCAATACAGACAAATGTGAAGC 417
QY 241 CAAAGTGGATTATCTCTGCACTCAGGCAGCTCTTTCCGGTGGTAAACAAGTTTGA 300
DB 418 CAAAGTGGATTATCTCTGCACTCAGGCAGCTCTTTCCGGTGGTAAACAAGTTTGA 477
QY 301 GCGCTGACAGTTGTATCCAGACACTCTCTGTGAGGGGGAGGAGCACTGAGAGCAC 360
DB 478 GCGCTGACAGTTGTATCCAGACACTCTCTGTGAGGGGGAGGAGCACTGAGAGCAC 537

QY 361 AAAACCCCTCTCTCAAGAACTTGTCAAGCTCCGGGGAGAGCTAGTTGCTGTCTCAAGGCC 420
DB 538 AAAACCCCTCTCTCAAGAACTTGTCAAGCTCCGGGGAGAGCTAGTTGCTGTCTCAAGGCC 597
QY 421 TGTGAGAGCTAGAAAAGCTAGGGCTGACTTACAGACAGCGGTATCAAGAAATTTGCCAG 480
DB 598 TGTGAGAGCTAGAAAAGCTAGGGCTGACTTACAGACAGCGGTATCAAGAAATTTGCCAG 657
QY 481 AACTAAACCGAGAGCATCAAGACAGCCGAGCGGAACTGGAGAACCGGCTCAAGAGCTTA 540
DB 658 AACTAAACCGAGAGCATCAAGACAGCCGAGCGGAACTGGAGAACCGGCTCAAGAGCTTA 717
QY 541 TACACCGCAGAGTGTGAGAACTTACAGCAATTTACATTGAGGAGCGCAAGAAATATAA 600
DB 718 TACACCGCAGAGTGTGAGAACTTACAGCAATTTACATTGAGGAGCGCAAGAAATATAA 777
QY 601 ACTCAACTGCAAGAGCGATTTGACAACCTTAAACGCGCGCCCATGAGACCACTTAAGCTTGAG 660
DB 778 ACTCAACTGCAAGAGCGATTTGACAACCTTAAACGCGCGCCCATGAGACCACTTAAGCTTGAG 837
QY 661 ATTGAAGCTAGCCACTCGGAGAGGCTGGAATTTGCTGAAGAGACCTATGAAACCTCCCTT 720
DB 838 ATTGAAGCTAGCCACTCGGAGAGGCTGGAATTTGCTGAAGAGACCTATGAAACCTCCCTT 897
QY 721 TCAGAAATCAAGAGAGCCATGAGATGGAGAAAGTCACTGGAGGATCTGCTTAATGAG 780
DB 898 TCAGAAATCAAGAGAGCCATGAGATGGAGAAAGTCACTGGAGGATCTGCTTAATGAG 957
QY 781 AAGCAGGATCGCTGAGAGAAACAAATCAATGATCTGAAGAGTGAAGAGTTCCTTTAAAC 840
DB 958 AAGCAGGATCGCTGAGAGAAACAAATCAATGATCTGAAGAGTGAAGAGTTCCTTTAAAC 1017
QY 841 GAAAGTTTCAATCAGAGAGGCAAAAGCACTGTCAAGAGAGAGAGGCGAATTCGAAAC 900
DB 1018 GAAAGTTTCAATCAGAGAGGCAAAAGCACTGTCAAGAGAGAGAGGCGAATTCGAAAC 1077
QY 901 CCTCAGTCAATGTATCTGGAAGCAAACTAGAAAGCCTGAAGGCTGTGTAGAGATCAAT 960
DB 1078 CCTCAGTCAATGTATCTGGAAGCAAACTAGAAAGCCTGAAGGCTGTGTAGAGATCAAT 1137
QY 961 AATGAGAGCTGCACAGAGAGCATGAGAGCTTAATGAAGTGAAGAGCTGGTGGAGCAAT 1020
DB 1138 AATGAGAGCTGCACAGAGAGCATGAGAGCTTAATGAAGTGAAGAGCTGGTGGAGCAAT 1197
QY 1021 AACACAGCAATTTGTTGACAAAGCTGAGCGAATTCAGCAGAGCAAAAGCGAGAGTTAAAGCT 1080
DB 1198 AACACAGCAATTTGTTGACAAAGCTGAGCGAATTCAGCAGAGCAAAAGCGAGAGTTAAAGCT 1257
QY 1081 CGCATGGACAAACATGGCAATTTCAAGGCAACTTTCCACGAGAGCGCGGCTGCAA 1140
DB 1258 CGCATGGACAAACATGGCAATTTCAAGGCAACTTTCCACGAGAGCGCGGCTGCAA 1317
QY 1141 GAGTCCCTTGAAGAGAGTCAAGGTCACAAAGAGACTGTCCATGGAAGAGAGACTT 1200
DB 1318 GAGTCCCTTGAAGAGAGTCAAGGTCACAAAGAGACTGTCCATGGAAGAGAGACTT 1377

QY 1201 CTGTGGAAACTGCACAAAGGAGACCTGTGCAGCCCCCAAGAGATCCCCCACTCCTCGGCC 1230
DB 1378 CTGTGGAAACTGCACAAAGGAGACCTGTGCAGCCCCCAAGAGATCCCCCACTCCTCGGCC 1431
QY 1261 ATCCCTTTCCAGTCCCCCAGGAATTCGGTTCCTTCTCCAGCCCCCAGCATCTCACCCAGA 1320
DB 1438 ATCCCTTTCCAGTCCCCCAGGAATTCGGTTCCTTCTCCAGCCCCCAGCATCTCACCCAGA 1497
QY 1321 TGA 1323
DB 1498 TGA 1500

Search completed: October 21, 2003, 11:11:03
Job time : 259.382 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 : Search time 270.694 Seconds
(without alignments)
13107.130 Million cell updates/sec

Title: US-09-762-194-3
Perfect score: 1323
Sequence: 1 atgtgtgtgtctcccaatt.....ccagcatctccacagatga 1323

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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1 865.4 65.4 4937 13 US-10-044-090-76 Sequence 76, Appl
2 644.8 48.7 910 14 US-10-043-487-47 Sequence 47, Appl
3 342.2 25.9 656 10 US-09-764-864-757 Sequence 757, App
4 304.6 23.0 481 10 US-09-764-864-342 Sequence 342, App
5 271.4 20.5 490 11 US-09-918-995-5132 Sequence 5132, App
6 212.8 16.1 435 10 US-09-983-965-3690 Sequence 3690, App
7 159.4 12.0 444 11 US-09-918-995-12481 Sequence 12481, A
8 156.8 11.9 1117 13 US-10-027-632-85144 Sequence 85144, A
9 131.8 10.0 440 11 US-09-918-995-11578 Sequence 11578, A
10 119.6 9.0 464 11 US-09-918-985-5569 Sequence 5569, App
11 104.2 7.9 133 10 US-09-998-598-2218 Sequence 2218, App
12 91.4 6.9 567 9 US-09-925-302-132 Sequence 132, App
13 67 5.1 3489 12 US-10-294-804-1 Sequence 1, Appl
14 55.2 4.2 628 12 US-10-029-386-22859 Sequence 22859, A
15 54.4 4.1 536 12 US-10-029-386-19974 Sequence 19974, A
16 54.4 4.1 599 12 US-10-029-386-6243 Sequence 6243, App
17 54.2 4.1 32069 12 US-10-004-113-7 Sequence 7, Appl
18 51.8 3.9 720 13 US-10-101-487-74 Sequence 74, Appl
19 51.8 3.9 720 13 US-10-101-487-76 Sequence 76, Appl
20 50.2 3.8 575 9 US-09-864-761-20733 Sequence 20733, A
21 50.2 3.8 1969 9 US-09-864-761-3972 Sequence 3972, App
22 49.8 3.8 8895 9 US-09-764-853-887 Sequence 887, App
23 49.8 3.8 8895 9 US-09-764-853-937 Sequence 937, App
24 49.8 3.8 8895 14 US-10-091-438-250 Sequence 250, App
25 49.8 3.8 8895 14 US-10-091-438-256 Sequence 256, App
26 49.8 3.8 9656 9 US-09-764-853-856 Sequence 856, App
27 49.8 3.8 9656 9 US-09-764-853-933 Sequence 933, App
28 49.8 3.8 9656 14 US-10-091-438-246 Sequence 246, App
29 49.8 3.8 9656 14 US-10-091-438-255 Sequence 255, App
30 49.6 3.7 423 9 US-09-864-761-18355 Sequence 18355, A
31 49.4 3.7 475 9 US-09-864-761-6203 Sequence 6203, App
32 49.4 3.7 511 9 US-09-864-761-22817 Sequence 22817, A
33 48.2 3.6 2313 10 US-09-738-973-157 Sequence 157, App
34 48.2 3.6 2313 10 US-09-854-133-157 Sequence 157, App
35 48.2 3.6 2313 14 US-10-144-649A-157 Sequence 157, App
36 48.2 3.6 2314 10 US-09-764-868-12 Sequence 12, Appl
37 48.2 3.6 2802 12 US-10-233-045-35 Sequence 35, Appl
38 47 3.6 3809 13 US-10-001-870-68 Sequence 68, Appl
39 46.6 3.5 541 12 US-10-029-386-12333 Sequence 12333, A
40 46.6 3.5 1040 12 US-10-029-386-26033 Sequence 26033, A
41 46.6 3.5 1371 10 US-09-938-842A-85 Sequence 85, Appl
42 46.2 3.5 700 9 US-09-864-761-17529 Sequence 17529, A
43 46 3.5 6668 12 US-10-311-455-1670 Sequence 1670, App
44 45.8 3.5 272 9 US-09-864-761-18684 Sequence 18684, A
45 45.6 3.4 659158 10 US-09-771-208-20 Sequence 20, Appl

Search completed: October 22, 2003, 03:34:41
Job time : 273.694 secs

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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 2085.84 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-3

Perfect score: 1323

Sequence: 1 atgtgtgtgtctccaaatt.....ccagcatctaccagatga 1323

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152236056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

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6: em_estpl:*

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8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310.2	99.0	2477	11	AK030510 Mus muscu
2	1292.6	97.7	3963	11	AK031693 Mus muscu
3	982.6	74.3	3237	11	AK035576 Mus muscu
4	896.6	67.8	950	13	BQ921402 AGNCOURT
5	604.4	45.7	657	10	BB628131 BB628131
6	603.2	45.6	1005	13	BQ070423 AGNCOURT
7	595.2	45.0	748	10	BF141309 AGNCOURT
8	592.4	44.7	624	12	BM951991 UI-M-EHO-
9	590.4	44.6	920	13	BQ523654 AGNCOURT
10	579.6	43.8	782	13	BQ702398 UI-M-F10-
11	567.4	42.9	734	14	CB316595 AGNCOURT
12	564.6	42.7	600	13	BQ921755 6093-85 M
13	538.4	40.7	541	4	BX512030 RZPD Mus
14	518.4	39.2	782	9	AU141757 AU141757
15	516.39	39.0	1346	11	BC007328 Homo sapi
16	515.8	39.0	830	9	AU138373 AU138373
17	513.8	38.8	517	10	BE652532 UI-M-AMO-
18	510.6	38.6	530	13	BQ830956 LL6in1027
19	508.6	38.4	710	14	CB723104 UI-M-GHO-
20	508.4	38.4	560	14	CD565243 B0491H11-
21	502.8	38.0	509	12	BI319660 lei4a05.Y
22	498.4	37.7	500	9	AA880300 vx39f05.r
23	485.4	36.7	487	10	BF535672 602054069
24	480	36.3	778	10	BE895149 601436077
25	463.4	35.0	474	9	AA980079 ua28c11.r
26	463.4	35.0	712	10	BB567855 BB567855
27	451.6	34.1	626	12	BM737916 K-EST006
28	445.2	33.7	450	14	CA556858 K0219E05-
29	441.8	33.4	758	10	BQ719490 602690048
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31	435	32.9	732	14	CB246442 UI-M-F10-
32	420.4	31.8	650	12	BM983699 UI-CF-DU1
33	419	31.7	510	13	BY000218 BY000218
34	418.4	31.6	600	12	BM311947 BM311947
35	415.6	31.4	776	13	BQ387252 603858971
36	389.6	29.4	862	13	BQ248050 603781419
37	383	28.9	557	10	BE552421 hw2602.x
38	380	28.7	380	10	BE449013 ut85q01.Y
39	380	28.7	573	12	BE536537 393580 MA
40	373.8	28.3	645	13	BQ549647 ik89f06.x
41	369.6	27.9	990	13	BQ893803 AGNCOURT
42	364	27.5	820	13	BQ344537 603522603
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44	362.8	27.4	648	10	BB656106 BB656106
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ALIGNMENTS

RESULT 1	AK030510	2477 bp	mRNA	linear	HTC 05-EE -2002
LOCUS	AK030510				
DEFINITION	Mus musculus adult male pituitary gland cDNA, RIKEN full-length cDNA library, clone:530423L05 product:TRANSCRIPTION FACTOR homolog [Homo sapiens], full insert sequence.				
ACCESSION	AK030510				
VERSION	AK030510.1 GI:26326504				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Math. Enzymol. 303, 19-44 (1999)				
MEDLINE	9279263				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, H., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamamoto, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Geasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, J., Washio, T., Sakai, K., Okidori, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,				

Fletcher,C., Fujita,M., Gariboldi,M., Gustinchich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Rongwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,K., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weiss,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
MEDLINE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2477)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kuribara,C., Matsuyama,I., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
JOURNAL cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
COMMENT Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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ORIGIN

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Matches 1315; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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homolog [Homo sapiens], full insert sequence.
AK031693
ACCESSION AK031693.1 GI:26327546
VERSION HTC; CAP trapper.
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SOURCE Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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Genome Res. 10 (10), 1617-1630 (2000)
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Shibata,K., Itoh,M., Aizawa,K., Nagacka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,I., Harada,A.,
Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishi.Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamakita,I.,
Saito,T., Okazaki,Y., Gojohori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
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Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
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Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,J.,
Ring,B., Ringwald,M., Rodriguez,L., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seva,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyochika,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

TITLE
JOURNAL
MEDLINE
PubMed
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3963)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,K., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,K., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission

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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pi:
9: gb_pr:
10: gb_rc:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_nu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:

28: em_un:
29: em_vi:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rod:
36: em_htg_man:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	354	100.0	1323	10 AY246699	AY246699 Mus muscu
2	354	100.0	1803	10 AF173380	AF173380 Mus muscu
3	354	100.0	3629	10 BC043321	BC043321 Mus muscu
4	354	100.0	5218	10 BC041777	BC041777 Mus muscu
5	354	100.0	5219	10 BC042206	BC042206 Mus muscu
6	312.4	88.2	1323	10 AY208915	AY208915 Rattus no
7	246.8	69.7	1142	9 BC017740	BC017740 Homo sapi
8	246.8	69.7	1615	6 AX301208	AX301208 Sequence
9	246.8	69.7	1758	6 AX209989	AX209989 Sequence
10	246.8	69.7	1977	9 AF293357	AF293357 Homo sapi
11	246.8	69.7	3315	6 BD160624	BD160624 Primer fo
12	246.8	69.7	3315	9 AK024357	AK024357 Homo sapi
13	246.8	69.7	3455	9 AF121259	AF121259 Homo sapi
14	246.8	69.7	3654	6 AX209987	AX209987 Sequence
15	246.8	69.7	3813	6 AX210064	AX210064 Sequence
16	246.8	69.7	5799	6 AX210061	AX210061 Sequence
17	246.8	69.7	5857	9 AB033114	AB033114 Homo sapi
18	245.2	69.3	1191	6 AX209993	AX209993 Sequence
19	245.2	69.3	1458	6 AX209991	AX209991 Sequence
20	245.2	69.3	5214	9 HSM800681	AL096842 Homo sapi
21	232.4	65.6	3742	6 AX210037	AX210037 Sequence
22	225.4	63.7	830	6 BD149938	BD149938 Primer fo
23	206.6	58.4	2895	9 BC033842	BC033842 Homo sapi
24	154.4	43.6	775	6 AX210002	AX210002 Sequence
c 25	123.4	34.9	194355	2 AC116511	AC116511 Mus muscu
26	112.2	31.7	270745	2 AC097544	AC097544 Rattus no
27	98.6	27.9	1003	5 AF176665	AF176665 Xenopus l
28	85	24.0	600	6 AX210051	AX210051 Sequence
c 29	85	24.0	100000	9 ABC20864	AB020864 Homo sapi
30	85	24.0	131299	9 AF165145	AF165145 Homo sapi
31	85	24.0	171075	2 AC026842	AC026842 Homo sapi
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33	85	24.0	186901	2 AF267167	AF267167 Homo sapi

c 34 85 24.0 195290 9 AP006249 Homo sapi
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36 72.2 20.4 700 6 AX210050 Sequence
37 71.6 20.2 1479 9 BC032481
38 71.6 20.2 4021 9 AB016317
39 70.2 19.8 203 6 AX210030 Sequence
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41 57 16.1 147277 10 AL929001
c 42 56.8 16.0 7218 6 I66494
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44 54.6 15.4 4892 5 AB081562
c 45 54.4 15.4 185738 2 AC141179

ALIGNMENTS

RESULT 1
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LOCUS AY246699 1323 bp mRNA linear ROD 10-APR-2003
DEFINITION Mus musculus M1SG1 mRNA, complete cds.
ACCESSION AY246699
VERSION AY246699.1 GI:29725653
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1323)
AUTHORS Seibold,S., Wanner,C. and Galle,J.
TITLE Cloning and characterization of M1SG1
JOURNAL Unpublished
2 (bases 1 to 1323)
AUTHORS Seibold,S., Wanner,C. and Galle,J.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2003) Department of Medicine, University of
Wuerzburg, Josef Schneider Str 2, Wuerzburg 97080, Germany

FEATURES
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AF173380
LOCUS AF173380 1803 bp mRNA linear ROD 16-AUG-1999
DEFINITION Mus musculus angiotensin II AT2 receptor-interacting protein mRNA,
complete cds.
ACCESSION AF173380
VERSION AF173380.1 GI:5733813
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Molecular characterization of ATIP, a novel angiotensin II type 2
receptor-interacting protein
JOURNAL Unpublished
2 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1999) Institut Cochin de Genetique Moleculaire,
CNRS UPR415, 22, rue Mechain, Paris 75014, France
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 Db 973 GAGAAACAAATCAATGATCTGAAGAGTGAAAGATGCTTTAAACGAAAGTTG 1026
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 LOCUS Mus musculus expressed sequence A1481402, mRNA (cDNA clone
 DEFINITION MGC:49379 IMAGE:5366361), complete cds.
 ACCESSION BC043321
 VERSION BC043321.1 GI:27694046

KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3629)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,D.,
 Klautner,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,J.K.,
 Hopkins,R.F., Jordan,H., Moore,J., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvachenko,Y.,
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 Butterfield,J.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
 Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 2388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 3629)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 cDNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Steven
 Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jacqueline
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.lln.gov>
 Series: IRAC Plate: 86 Row: n Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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Best Local Similarity	100.0%; Pred. No. 2.3e-78;
Matches 354; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION	Mus musculus expressed sequence A1481402, mRNA (cDNA clone MGC:31380 IMAGE:4240274), complete cds.
ACCESSION	BC041777
VERSION	BC041777.1 GI:27469800
KEYWORDS	MGC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	1 (bases 1 to 5218)
AUTHORS	Klausner, R.D., Collins, F.S., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, K., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)
MEDLINE	22388257
PMID	12477932
REFERENCE	2 (bases 1 to 5218)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (23-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: gcgaps@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, J., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAC Plate: 43 Row: 0 Column: 3.

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KRSPTSSAIPFSPPNSGFSFSISPR"

BASE COUNT

1591 a 1192 c 1183 g 1262 t
ORIGIN
Query Match 100.0%; Score 354; DB 10; Length 5218;
Best Local Similarity 100.0%; Fred. No. 2.3e-78;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

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|||||

Db

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|||||
Db 2180 GAGAACAAATCAATGATCTGAAGAGTGAAACGATGCTTTAAACGAAAGTTG 2233
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RESULT 5
BC042206 5219 bp mRNA linear ROD 10-JUN-2003
LOCUS Mus musculus expressed sequence AI481402, mRNA (cDNA clone
MGC:49685 IMAGE:4240274), complete cds.

ACCESSION BC042206
VERSION BC042206.1 GI:27503397
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 5219)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22389257

TITLE

JOURNAL

MEDLINE

12477932

PUBMED

2 (bases 1 to 5219)

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (02-JAN-2003)

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center (NISC),

Gaithersburg, Maryland

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nigri.nih.gov

Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 85 Row: i Column: 19.

Location/Qualifiers

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REMARK

COMMENT

BASE COUNT

1581 a 1193 c 1183 g 1262 t

ORIGIN

Query Match

100.0%; Score 354; DB 10; Length 5219;

Best Local Similarity 100.0%; Pred. No. 2.3e-78;

Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATCAGACAGACCGGACGGAACCTGGAGACCGGCTGAAGGACTTATACACCGCAGAGTGT 60

DB 1880 CATCAGACAGACCGGACGGAACCTGGAGACCGGCTGAAGGACTTATACACCGCAGAGTGT 1939

QY 61 GAGAGCTTCAGACGATTACATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120

DB 1940 GAGAGCTTCAGACGATTACATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1999

QY 121 CAGTTTGCACACTTAAACGCCGCCCATGAGACCACTAGCTTGAGATTGAGCTAGCCAC 180

DB 2000 CAGTTTGCACACTTAAACGCCGCCCATGAGACCACTAGCTTGAGATTGAGCTAGCCAC 2059

QY 181 TCGGAGAGAGTGGAGTGTCTGAAGAGACCTATGAACCTCCCTTTCAGAAATCAAGAA 240

DB 2060 TCGGAGAGAGTGGAGTGTCTGAAGAGACCTATGAACCTCCCTTTCAGAAATCAAGAA 2119

QY 241 AGCATGAGATGGAGAGAGAGTCACTGGAGGATCTGCTTAATGAGACGAGGAGTGGT 300

DB 2120 AGCATGAGATGGAGAGAGAGTCACTGGAGGATCTGCTTAATGAGACGAGGAGTGGT 2179

QY 301 GAGAAACAAATCAATGATCTGAAGAGTGAACACGATGCTTTAAAGGAAAGGTTG 354

DB 2180 GAGAAACAAATCAATGATCTGAAGAGTGAACACGATGCTTTAAAGGAAAGGTTG 2233

Search completed: October 21, 2003, 17:17:55

Job time : 906.403 secs

FEATURES

source

gene

CDS

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:19 ; Search time 68.0658 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-5

Perfect score: 354

Sequence: 1 catcacagacaccgacgca.....atgcttttaacgaagggtg 354

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	354	100.0	354	21	Mouse ATIP coding
2	354	100.0	1323	21	Mouse ATIP coding
3	354	100.0	1803	21	Mouse ATIP gene.
4	246.8	69.7	481	25	Human cDNA encoding
5	246.8	69.7	481	25	Human novel polynu
6	246.8	69.7	910	24	Human cDNA encoding
7	246.8	69.7	1615	24	Polynucleotide enc
8	246.8	69.7	1758	22	Nucleotide sequenc
9	246.8	69.7	3315	22	Human cDNA sequenc
10	246.8	69.7	3654	22	Human cDNA sequenc
11	246.8	69.7	3807	25	Human cDNA encoding
12	246.8	69.7	4937	25	Human cDNA #76 dif
13	246.8	69.7	5961	22	Nucleotide sequenc
14	245.2	69.3	1191	22	Nucleotide sequenc
15	245.2	69.3	1369	22	Nucleotide sequenc
16	245.2	69.3	1458	22	Nucleotide sequenc
17	245.2	69.3	5799	22	Nucleotide sequenc
18	234	66.1	656	22	Human cDNA encoding
19	232.4	65.6	1308	25	Human novel polynu
20	232.4	65.6	3742	21	Human ATIP coding
21	232.4	65.6	3742	21	Human ATIP gene.
22	232.4	65.6	3742	22	Nucleotide sequenc
23	225.4	63.7	830	22	Human cDNA clone (
24	160.2	45.3	242	25	Human cDNA sequenc
25	154.4	43.6	775	22	Nucleotide sequenc
26	130	36.7	338	21	Human secreted exp
27	128	36.2	562	23	Human prostate exp
28	104.2	29.4	133	24	Human colon cancer
29	96	27.1	791	25	Human genomic DNA
30	96	27.1	3287	21	Human secreted pro
31	85	24.0	600	22	Nucleotide sequenc
32	82	23.2	106	22	Nucleotide sequenc
33	72.2	20.4	700	22	Nucleotide sequenc
34	71.6	20.2	4184	25	Novel human cDNA s
35	70.2	19.8	203	22	Nucleotide sequenc
36	53	15.0	435	22	Nucleotide sequenc
37	50.8	14.4	540	23	Human prostate exp
38	50	14.1	74	22	Nucleotide sequenc
39	45.2	12.8	458	22	Nucleotide sequenc
40	44.6	12.6	1080	24	Mouse ischaemic co
41	43.6	12.3	1563	24	Nucleotide sequenc
42	43	12.1	96	22	Nucleotide sequenc
43	42.2	11.9	843	23	DNA encoding novel
44	42	11.9	240	23	Drosophila melanog
45	42	11.9	2240	23	Drosophila melanog

ALIGNMENTS

RESULT 1

AAZ99090

ID AAZ99090 standard; cDNA; 354 BP.

XX

AC AAZ99090;

XX

DT 21-JUN-2000 (first entry)

XX

DE Mouse ATIP coding sequence probe.

XX

KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;

KW two-hybrid screen; signal transduction; hybridisation probe.

XX

OS Mus sp.

XX

PN FR2782084-A1.

XX

PD 11-FEB-2000.

XX

PF 04-AUG-1998; 98FR-0009997.

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PR 04-AUG-1998; 98FR-0009997.

XX

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Elbaz N, Nahmias C, Strosberg AD;

XX

DR WPI: 2000-248410/22.

DR P-PSDB; AAY83779.

XX

PT Nucleic acids coding for angiotensin II receptor AT2 interacting

PT proteins useful in screening assays for receptor-protein interaction -

XX

PS Claim 1; Page 33-34; 63pp; French.

XX

CC This sequence represents the initial clone for the cDNA encoding a mouse

CC angiotensin II (AT2) receptor interactive protein (ATIP; AAY83777). The

CC sequence was subsequently used as a hybridisation probe to isolate the

CC complete gene (AAZ99090) from a two-hybrid screen using the C-terminal

CC fragment of the mouse AT2 receptor as the "bait" (AAY83781). The

CC "target" is a mouse foetal cDNA library. Cells transformed with vectors

CC containing the cDNA, or immobilized proteins encoded by it, can be used

CC to screen for substances that modulate ATIP-AT2 interaction or substances

CC that interact with ATIP, especially using yeast two- or three-hybrid

CC techniques. Such substances may be useful for treating disorders

CC associated with anomalous AT2 receptor signal transduction.

XX

SQ Sequence 354 BP; 130 A; 67 C; 92 G; 65 T; 0 other;

Query Match 100.0%; Score 354; DB 21; Length 354;

Best Local Similarity 100.0%; Pred. No. 7.2e-89;

Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAGAGCTTCAGAGCATTTACATTGAGGAGCGAGAAATATATAAACTCAACTGCGAGAG 120

DB 61 GAGAGCTTCAGAGCATTTACATTGAGGAGCGAGAAATATATAAACTCAACTGCGAGAG 120

QY 121 CAGTTTGACAACTTTAAACGCGCCCATGAGACCACTAAGCTTGAGATTGAGGTAGCCAC 180

DB 121 CAGTTTGACAACTTTAAACGCGCCCATGAGACCACTAAGCTTGAGATTGAGGTAGCCAC 180

QY 181 TCGGAGAGGTGGAAATGCTGAAGAGACCTATGAACCTCCCTTCAGAAATCAAGAG 240

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DB 241 AGCCATGAGATGGAGAGAGTCACTGAGGATCTGCTTAATGAGAGCGAGGATCGCT 300

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DB 301 GAGAAACAAATCAATGATCTGAAGAGTGAAACGATGCTTTAAACGAAAGGTTG 354

RESULT 2

AAZ99089

ID AAZ99089 standard; cDNA; 1323 BP.

XX

AC AAZ99089;

XX

DT 21-JUN-2000 (first entry)

XX

DE Mouse ATIP coding sequence.

XX

KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;

KW two-hybrid screen; signal transduction; coding sequence.

XX

OS Mus sp.

XX

PN FR2782084-A1.

XX

PD 11-FEB-2000.

XX

PF 04-AUG-1998; 98FR-0009997.

XX

PR 04-AUG-1998; 98FR-0009997.

XX

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Elbaz N, Nahmias C, Strosberg AD;

XX

DR WPI: 2000-248410/22.

DR P-PSDB; AAY83777.

XX

PT Nucleic acids coding for angiotensin II receptor AT2 interacting

PT proteins useful in screening assays for receptor-protein interaction -

XX

PS Claim 1; Page 30-31; 63pp; French.

XX

CC This sequence represents the open reading frame (ORF) of the cDNA
 CC encoding a mouse angiotensin II (AT2) receptor interactive protein
 CC (ATIP). The gene was isolated from a two-hybrid screen using the
 CC C-terminal fragment of the mouse AT2 receptor as the "bait" (AAY83781).
 CC The "target" is a mouse foetal cDNA library. Cells transformed with
 CC vectors containing the cDNA, or immobilized proteins encoded by it,
 CC can be used to screen for substances that modulate ATIP-AT2 interaction
 CC or substances that interact with ATIP, especially using yeast two- or
 CC three-hybrid techniques. Such substances may be useful for treating
 CC disorders associated with anomalous AT2 receptor signal transduction.
 XX
 XX Sequence 1323 BP; 425 A; 326 C; 325 G; 247 T; 0 other;
 SQ

Query Match 100.0%; Score 354; DB 21; Length 1323;
 Best Local Similarity 100.0%; Pred. No. 1.1e-88;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATCAGACAGACCGGACGGAAGTGGAGAACCGGCTGAAGGACTTATACACCGCAGAGTGT 60
 DB 496 CATCAGACAGACCGGACGGAAGTGGAGAACCGGCTGAAGGACTTATACACCGCAGAGTGT 555
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 DB 616 CAGTTTGACACCTTAAACGGCGCCATGAGACCACTAAGCTTGAGATTGAAGCTAGCCAC 675
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RESULT 3
 ID AAZ99088 standard; cDNA; 1803 BP.
 AC
 XX
 XX AAZ99088;
 DT 21-JUN-2000 (first entry)
 XX
 XX Mouse ATIP gene.
 DE
 XX
 KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
 KW two-hybrid screen; signal transduction.
 XX
 CS Mus sp.
 XX

FH Key Location/Qualifiers
 FT 178
 FT /tag= a
 FT /product= "ATIP"
 FT /note= "angiotensin II (AT2) receptor interactive
 protein"
 XX
 PN FR2782084-A1.
 XX
 PD 11-FEB-2000.
 XX
 XX 04-AUG-1998; 98FR-0009997.
 XX
 PR 04-AUG-1998; 98FR-0009997.
 XX
 PA (QNSR) QNSR CENT NAT RECH SCI.
 XX
 PI Elbaz N, Nahmias C, Strosberg AD;
 XX
 DR WPI; 2000-248410/22.
 XX
 XX P-PSDB; AAY83777.
 DR
 XX Nucleic acids coding for angiotensin II receptor AT2 interacting
 PT proteins useful in screening assays for receptor-protein interaction -
 XX
 PS Claim 1; Fig 3; 63pp; French.
 XX
 CC This sequence represents the cDNA encoding a mouse angiotensin II (AT2)
 CC receptor interactive protein (ATIP). The gene was isolated from a
 CC two-hybrid screen using the C-terminal fragment of the mouse AT2
 CC receptor as the "bait" (AAY83781). The "target" is a mouse foetal cDNA
 CC library. Cells transformed with vectors containing the cDNA, or
 CC immobilized proteins encoded by it, can be used to screen for substances
 CC that modulate ATIP-AT2 interaction or substances that interact with
 CC ATIP, especially using yeast two- or three-hybrid techniques. Such
 CC substances may be useful for treating disorders associated with anomalous
 CC AT2 receptor signal transduction.
 XX
 SQ Sequence 1803 BP; 539 A; 464 C; 440 G; 360 T; 0 other;

Query Match 100.0%; Score 354; DB 21; Length 1803;
 Best Local Similarity 100.0%; Pred. No. 1.3e-88;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATCAGACAGACCGGACGGAAGTGGAGAACCGGCTGAAGGACTTATACACCGCAGAGTGT 60
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 QY 61 GAGAAGCTTCAGAGCATTTACATTGAGGAGCGAGAAATATAAACTCAACTGCAAGAG 120
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 QY 181 TCGGAGAGGTGGAATTGCTGAGAGACCTATGAAACGATGCTTTAAACGAAAGGTTG 240

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QY 241 AGCCATGAGATGAGAGAGTCACTGGAGATCTGCTTAATGAGAGCGAGGAATCGCTG 300
Db 913 AGCCATGAGATGAGAGAGTCACTGGAGATCTGCTTAATGAGAGCGAGGAATCGCTG 972
QY 301 GAGAAACAATCAATGATCTGAAGAGTGAAGACGATGCTTTAAACGAAAGGTTG 354
Db 973 GAGAAACAATCAATGATCTGAAGAGTGAAGACGATGCTTTAAACGAAAGGTTG 1026

Search completed: October 21, 2003, 11:11:04
Job time : 69.0658 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 72.4306 Seconds
(without alignments)
13107.130 Million cell updates sec

Title: US-09-762-194-5
Perfect score: 354
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5 194.8 55.0 490 11 US-09-918-995-3132
6 104.2 29.4 133 10 US-09-998-598-2218
7 43 12.1 32069 12 US-10-004-113-7
8 42.2 11.9 536 12 US-10-029-386-19974
9 42.2 11.9 599 12 US-10-029-386-6243
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14 38.2 10.8 511 9 US-09-864-761-22817
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Sequence 5132, Ap
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Job time : 560.115 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 9570.68 Seconds
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Title: US-09-762-194-7
Perfect score: 3742
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2885711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 40 650.2 17.4 897 6 BD097982 BD097982 Novel gen
41 545.2 14.6 270745 2 AC097544 AC097544 Rattus no
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 53 from Patent WO0157209.
ACCESSION AX210037
VERSION AX210037.1 GI:15424423
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Nahmias,C., Strosberg,A.D. and Nouet,S.
TITLE Novel family of proteins, called atip, nucleic sequences coding for same and thereof
JOURNAL Patent: WO 0157209-A 53 09-AUG-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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Best Local Similarity 100.0%; Pred. No. 0;

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Db TTTT|||||TT
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QY TTTT|||||TT
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Db TTTT|||||TT
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3541 AAGATGGGAAACAAATAGAGATTCTTAAGATTTTGGTTTAAACCAATGTTTCATGTAG 3600
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Db TTTT|||||TT
3721 AAAAAAAAAAAAAAAAAAAAAA 3742

Search completed: October 21, 2003, 17:18:05
Job time : 9580.68 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:18 ; Search time 719.498 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-7
Perfect score: 3742
Sequence: 1 cagtgtgatgtgttcagag.....aaaaaaaaaaaaaaaaaaaa 3742

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	3742	21	AAZ99091 Human ATIP gene.
2	3742	100.0	3742	22	AAH74362 Nucleotide sequence
3	3267	87.3	3315	22	AAH18632 Human cDNA sequence
4	3251.6	86.9	4937	25	ABX63076 Human cDNA #76 dif
5	3250.6	86.9	5799	22	AAH74363 Nucleotide sequence
6	3249	86.8	5961	22	AAH74385 Nucleotide sequence
7	2473.4	66.1	3287	21	AAF22392 Human secreted pro
8	2313.2	61.8	2850	22	AAH74380 Nucleotide sequence
9	2305.8	61.6	2333	22	AAH74361 Nucleotide sequence
10	1774	47.4	2015	23	ABV25051 Human prostate exp
11	1594.2	42.6	1615	24	AAZ99095 Polynucleotide enc
12	1308	35.0	1308	21	AAZ99092 Human ATIP coding
13	1290.2	34.5	1369	22	AAH74322 Nucleotide sequence
14	1187.8	31.7	3807	25	ABX10230 Human cDNA encodin
15	1177.4	31.5	1758	22	AAH74324 Nucleotide sequence
16	1177.4	31.5	3654	22	AAH74323 Nucleotide sequence
17	1175.8	31.4	1458	22	AAH74325 Nucleotide sequence
18	1173.4	31.4	1191	22	AAH74326 Nucleotide sequence
19	1051	28.1	1803	21	AAZ99088 Mouse ATIP gene.
20	941.8	25.2	1323	21	AAZ99089 Human cDNA encodin
21	894	23.9	910	24	ABX51467 Nucleotide sequence
22	773.4	20.7	775	22	AAH74327 Human cDNA clone (
23	740	19.8	830	22	AAH07946 Human neuroblastom
24	658.8	17.6	888	22	AAI94206 Human colon cancer
c 25	650.2	17.4	897	22	AAH33059 Human cDNA encodin
c 26	519.2	13.9	581	22	AAH33059 Human cDNA encodin
27	509.2	13.6	656	22	AAZ26578 Human novel polynu
c 28	509.2	13.6	656	25	ABX73919 Human cDNA clone (
29	483.8	12.9	505	22	AAH12914 Human genomic DNA
30	457.6	12.2	791	25	AAZ53121 Human cDNA encodin
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32	443.6	12.0	481	25	ABX73504 Nucleotide sequence
c 33	413.4	11.0	900	22	AAH74371 cDNA encoding huma
c 34	413.4	11.0	2672	24	ABK09997 Nucleotide sequen
35	413	11.0	413	22	AAH74352 Gene #1238 used i
c 36	366	9.8	366	24	ABN94740 Thyroid cancer re
c 37	366	9.8	366	24	ABL67318 Human secreted pr
38	327.4	8.7	330	21	AAH18620 Nucleotide sequence
39	312.8	8.4	367	22	AAH74329 Human prostate exp
40	285.8	7.6	389	23	ABV37795 Human secreted pro
41	241	6.4	253	21	AAZ09266 Human cDNA sequenc
c 42	234.6	6.3	242	25	ABX74609 Mouse ATIP coding
43	232.4	6.2	354	21	AAZ99090 Nucleotide sequenc
44	218	5.8	700	22	AAH74372 Nucleotide sequenc
45	215	5.7	215	22	AAH74353

ALIGNMENTS

RESULT 1
AAZ99091
ID AAZ99091 standard; cDNA; 3742 BP.
XX
AC AAZ99091;
XX 21-JUN-2000 (first entry)
XX Human ATIP gene.
DE Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
KW two-hybrid screen; signal transduction; human.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
CDS 293..1600
FT /*tag= a
FT /product= "human ATIP"
FT /note= "angiotensin II (AT2) receptor interactive
protein"
XX FR2782084-A1.
XX 11-FEB-2000.
XX 04-AUG-1998; 98FR-0009997.
XX 04-AUG-1998; 98FR-0009997.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX Elbaz N, Nahmias C, Strosberg AD;
XX WFI; 2000-248410/22.
XX P-PSDB; AAY83780.
XX Nucleic acids coding for angiotensin II receptor AT2 interacting
XX proteins useful in screening assays for receptor-protein interaction -
XX Claim 1; Fig 4; 63pp; French.
XX This sequence represents the cDNA encoding a human angiotensin II (AT2)
XX receptor interactive protein (ATIP). The gene was isolated using a
XX fragment of the mouse gene (AAZ99088). Cells transformed with vectors
XX containing the cDNA, or immobilized proteins encoded by it, can be used
XX to screen for substances that modulate ATIP-AT2 interaction or
XX substances that interact with ATIP, especially using yeast two- or
XX three-hybrid techniques. Such substances may be useful for treating
XX disorders associated with anomalous AT2 receptor signal transduction.
XX
SQ Sequence 3742 BP; 1180 A; 762 C; 793 G; 1007 T; 0 other;

Query Match 100.0%; Score 3742; DB 21; Length 3742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	901	TGACAACTTAATGGGCATGAATCCTCTAGTTTGGAAATGAAGCTAGCCATCAGAGAA	960
DB	901	TGACAACTTAATGGGCATGAATCCTCTAGTTTGGAAATGAAGCTAGCCATCAGAGAA	960
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DB	961	ACTTGAATTCCTTAAGAAAGGCGCTATGAAGCGTCCTTTTCAAAATTAAGAAAGGCCATGA	1020
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DB	1021	AATGAAAGAAATCGCTCGAGATTTACTTTCTGAGAGCGAGAAATCGCTAGAGAGCA	1080
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DB	1081	AATCAATGATCTGAAGAGTGAATATGATGCTTTAAATGAAATTTGAATTCAGAGAAACA	1140
QY	1141	AAAAGAAGCGCAGAGAAAGCAATTTGAAAATTCCTCAGATCATGTATCTAGAAACA	1200
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DB	1201	GGAGTTAGAAAAGCCTGAAAGCTGTGTAGAGATCAAGAAATGAGAACTCATCACAGGA	1260
QY	1261	CATCAAGTTAATGAAATCGAGAACTGGTGGACACAACACAGCATTTGTTTGACAAAT	1320
DB	1261	CATCAAGTTAATGAAATCGAGAACTGGTGGACACAACACAGCATTTGTTTGACAAAT	1320
QY	1321	GAAAGGTTTCAGCAGAGGAATGAAGAAATGAAGCTCGGATGGACAGGCATGGGAA	1380
DB	1321	GAAAGGTTTCAGCAGAGGAATGAAGAAATGAAGCTCGGATGGACAGGCATGGGAA	1380
QY	1381	CTCAAGCGAGCTTTCCAGCGAGCAGGCTGCTCTCAAGAGTCGCTGGAGAAGAGTGGAA	1440
DB	1381	CTCAAGCGAGCTTTCCAGCGAGCAGGCTGCTCTCAAGAGTCGCTGGAGAAGAGTGGAA	1440
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QY 3721 AAAAAAAAAAAAAAAAAAAAAA 3742
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Db 3721 AAAAAAAAAAAAAAAAAAAAAA 3742
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RESULT 2
AAH74362
ID AAH74362 standard; DNA; 3742 BP.
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AC AAH74362;
XX
DT 15-OCT-2001 (first entry)
XX
DE Nucleotide sequence of a human ATIP isoform, designated hATIP1.
XX
KW Human; ATIP; hATIP2; hATIP3; hATIP4; hATIP5; hATIP6; AT2 receptor;
KW angiotensin II receptor; antioncogenic; 8p21.3-p22; cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 293..1600
FT /*tag= a
FT /product= "hATIP1"
XX
PN W0200157209-A2.
XX
PD 09-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-FR00359.
XX
PR 07-FEB-2000; 2000FR-0001504.
XX
PA (CHRS) CNRS CENT NAT RECH SCI.
XX
PI Nahmias C, Stresberg AD, Nouet S;

XX WPI; 2001-48880/53.
DR P-PSDB; AAG63540.
XX
PT New protein family, designated hATIP, which interacts with the AT2
PT receptor of angiotensin II are anti-oncogenic and useful to detect and
PT treat cancer or precancerous conditions -
XX
PS Claim 11; Page 106-109; 118pp; French.
XX
CC The present sequence encodes an isoform of the human ATIP protein,
CC designated hATIP1. ATIP has isoforms designated hATIP2, hATIP3, hATIP4,
CC hATIP5 and hATIP6. All ATIP proteins comprise in their C-terminals
CC a common fragment which interacts with the angiotensin II (AT2)
CC receptor. ATIP proteins have antioncogenic functions. The human ATIP
CC gene has 17 exons, and is located at chromosome region 8p21.3-p22.
CC ATIP polynucleotides and polypeptides are used to detect, evaluate or
CC give prognosis for a cancer or pre-cancer condition, and as an
CC anti-tumour medication.
XX
SQ Sequence 3742 BP; 1180 A; 762 C; 793 G; 1007 T; 0 other;
Query Match 100.0%; Score 3742; DB 22; Length 3742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 1 CAGTGTGATGTGGTTCAGAGCGAGCTTCTAGACCTGCAGAGGAGAGATTGTATTCAAGG 60
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QY 61 AAGAGCATCATTTTGGCAACATCTGAAAGTGAACGAGAGCCAGAACACTTGGCCAG 120
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Db 121 CCTGGGGGATTTTCTCTATGCCTCTGTGTGGTGAATGACATTTGCTGTAGGCAAT 180
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Db 181 TTTCTCTGACTGTATTCTTGGCCTTGAAGAGTACTGAGTTTAAAGAGACAGTATGTGA 240
|||||
QY 241 CAGTCCATGGAATTTGCCTCTCTGTGAAATCTGCACCTGCTCCGAGACAGATGTGTT 300
|||||
Db 241 CAGTCCATGGAATTTGCCTCTCTGTGAAATCTGCACCTGCTCCGAGACAGATGTGTT 300
|||||
QY 301 GTCTCCCAAATTCCTTTATCCACATTCACATACGACTGAGGCCAAAGATTTGCTTCG 360
|||||
Db 301 GTCTCCCAAATTCCTTTATCCACATTCACATACGACTGAGGCCAAAGATTTGCTTCG 360
|||||
QY 361 AAACCTTCGACTTCCCTTCAGGGTTTAGGAGAGCACTGTGTGTTTCCACACAGTTGAAAA 420
|||||
Db 361 AAACCTTCGACTTCCCTTCAGGGTTTAGGAGAGCACTGTGTGTTTCCACACAGTTGAAAA 420
|||||
QY 421 GAGAGGCAAAAGATTCCTCGAGCTTATGTATCCAGCCACAGACAGCTCCGATGGCCT 480
|||||
Db 421 GAGAGGCAAAAGATTCCTCGAGCTTATGTATCCAGCCACAGACAGCTCCGATGGCCT 480
|||||

Qy	1321	GAAGCTTTCCACGAGGAGATGAAGAAATTGAAACTCGTGATGGACACAGCATGGGCA.	1380
Db	1321	GAAGCTTTCCACGAGGAGATGAAGAAATTGAAAGCTCGATGGACAGCAGCATGGCA.	1390
Qy	1381	CTCAAGGCAGCTTTCACCGGACAGGCTGTCTGCAAGAGTCGCTGGAGAAGAGTGG.	1440
Db	1381	CTCAAGGCAGCTTTCACGCGACAGGCTGTCTGCAAGAGTCGCTGGAGAAGAGTGGCA.	1440
Qy	1441	AGTCACAACGCCATCTCTATGGAAAACAAGAGSCTTCTGTGGAAACTGCACAAATGGGA	1500
Db	1441	AGTCACAACAGCATCTCTATGGAAAACAAGAGSCTTCTGTGAAACTGCACAAATGGGA	1500
Qy	1501	CCTGTGTAGCCCAAGAGATCCCGCACATCTCTCGSCCATCCCTTTCGAGTCAACCAGAA	1560
Db	1501	CCTGTGTAGCCCAAGAGATCCCGCACATCTCTCGSCCATCCCTTTCGAGTCAACCAGAA	1560
Qy	1561	TTCGGGCTCCCTTCCTTAGCCCCAGCATTTCACCCAGATGACAGTCCCCAAGTCCACAG	1620
Db	1561	TTCGGGCTCCCTTCCTTAGCCCCAGCATTTCACCCAGATGACAGTCCCCAAGTCCACAG	1620
Qy	1621	ACTCTCTGAAAGCATTTGATGCAAGTCTGCAAGACTGACCCCAAGAGAAAGTGGGA	1680
Db	1621	ACTCTCTGAAAGCATTTGATGCAAGTCTGCAAGACTGACCCCAAGAGAAAGTGGGA	1680
Qy	1681	CAAGAGTATATACGACACAGTGTGATCATCCGTAGTGTAACTGGAGGTCACCAACCGGG	1740
Db	1681	CAAGAGTATATACGACACAGTGTGATCATCCGTAGTGTAACTGGAGGTCACCAACCGGG	1740
Qy	1741	AATCGAGCTCTGAGACTGGAAGTCTGGAGAGAGACTTTTGCTCCGTCCAAAAGATCC	1800
Db	1741	AATCGAGCTCTGAGACTGGAAGTCTGGAGAGAGACTTTTGCTCCGTCCAAAAGATCC	1800
Qy	1801	TCGAAAAAAGATTTAAAAAAGATTTCCGCACTGACAGGAGCTTGTTCACACAAAGAC	1860
Db	1801	TCGAAAAAAGATTTAAAAAAGATTTCCGCACTGACAGGAGCTTGTTCACACAAAGAC	1860
Qy	1861	TTAAGAAGCAGAGCATCTTGTTCATTGCGTTTTTCACTTAAGCATTAAGGGGAAAACCTC	1920
Db	1861	TTAAGAAGCAGAGCATCTTGTTCATTGCGTTTTTCACTTAAGCATTAAGGGGAAAACCTC	1920
Qy	1921	TCAGGGGCCCTATTAGAAATTATACCTTTGTATGTTCTTCAACACAGACACCTCTTG.	1980
Db	1921	TCAGGGGCCCTATTAGAAATTATACCTTTGTATGTTCTTCAACACAGACACCTCTTG.	1980
Qy	1981	GAGTTTTCAGTCTGACGTGGGGTGGGGGTGTGAATGAATGATGTACAGAGTGT.	2040
Db	1981	GAGTTTTCAGTCTGACGTGGGGTGGGGGTGTGAATGAATGATGTACAGAGTGT.	2040
Qy	2041	ATGTGTCTGATCGAGCCTCCCTGCTGTGTATTAATGTCAAATCTGAATATATCTG.	2100
Db	2041	ATGTGTCTGATCGAGCCTCCCTGCTGTGTATTAATGTCAAATCTGAATATATCTG.	2100
Qy	2101	TATGTACTAATCAATAATATCAATCAATCAGCATATACATTTCAAGAACCATAGA	2160
Db	2101	TATGTACTAATCAATAATATCAATCAATCAGCATATACATTTCAAGAACCATAGA	2160
Qy	2161	AGAAAAAGCAATAGTCTGTTGAATTATGATCACTACACACCACTGTCTGACGCCCTGT	2220

Db 2161 AAAAAAGCAAGTTCCTGAAATATGATCATCTACCAAGCACTCTGTCAGCCCTGTA 2220
QY 2221 ACAGGTAGGGAGGGTATAACAGGAAGAGCTTTGACTTGTCCCTGCTATATACATCTC 2280
Db 2221 ACAGGTAGGGAGGGTATAACAGGAAGAGCTTTGACTTGTCCCTGCTATATACATCTC 2280
QY 2281 TGTATCTTTTGGGGTAACCTCTCTGGCAAGTTTTTCAAGTGTTCAGCCAGTGTGAGTGTGAGAC 2340
Db 2281 TGTATCTTTTGGGGTAACCTCTCTGGCAAGTTTTTCAAGTGTTCAGCCAGTGTGAGTGTGAGAC 2340
QY 2341 TAGATTTTCTGTAGATTTTCTTACCTATACCCATGTGAGCCTAACATCTCCTGTAAATCAT 2400
Db 2341 TAGATTTTCTGTAGATTTTCTTACCTATACCCATGTGAGCCTAACATCTCCTGTAAATCAT 2400
QY 2401 TTTCTCAGGCTATGTGAATGTAGAACCCCTAATTTTTCTATAAAAAACAACTAACTA 2460
Db 2401 TTTCTCAGGCTATGTGAATGTAGAACCCCTAATTTTTCTATAAAAAACAACTAACTA 2460
QY 2461 ACTGTGTAAAGAAAGAAAGGGAAGTACCAATGGGTTTTTCCACTATATTTTACCTTT 2520
Db 2461 ACTGTGTAAAGAAAGAAAGGGAAGTACCAATGGGTTTTTCCACTATATTTTACCTTT 2520
QY 2521 GATCTAGCCCTTGCAAGTTTAACTGTCTTCTTCCCTCCCATTAATCTCATTTTCCCTTTA 2580
Db 2521 GATCTAGCCCTTGCAAGTTTAACTGTCTTCTTCCCTCCCATTAATCTCATTTTCCCTTTA 2580
QY 2581 CCTTCTCCACATCCAGAGCCACAAAGCAACCTTCTACCTCTCCTACTACTTTTCTCT 2640
Db 2581 CCTTCTCCACATCCAGAGCCACAAAGCAACCTTCTACCTCTCCTACTACTTTTCTCT 2640
QY 2641 GGGACAAGGATAGGAATATGATTTTCCAGAGCCCCAGAGCCAGCTCATCTTCCAGGTG 2700
Db 2641 GGGACAAGGATAGGAATATGATTTTCCAGAGCCCCAGAGCCAGCTCATCTTCCAGGTG 2700
QY 2701 CTGAACCACTTTCCAAATAAACTAAAGCTTGATTTGATTAACAATTTTGGGAATC 2760
Db 2701 CTGAACCACTTTCCAAATAAACTAAAGCTTGATTTGATTAACAATTTTGGGAATC 2760
QY 2761 TTAGATAAGACGAGAACAGAGTCAATTTGGCTAGTATAATTAAGAAAGTAGATTT 2820
Db 2761 TTAGATAAGACGAGAACAGAGTCAATTTGGCTAGTATAATTAAGAAAGTAGATTT 2820
QY 2821 CAGTGTTCAGATGATGCACTACTTGATAGAAACAGCTCTGGAGAGTAGGCTCA 2880
Db 2821 CAGTGTTCAGATGATGCACTACTTGATAGAAACAGCTCTGGAGAGTAGGCTCA 2880
QY 2881 TTTTTCAGTTACCTTTAAGAGTCCCTTTGTTTGGGAAAGTAGCAGAAATGTCGCT 2940
Db 2881 TTTTTCAGTTACCTTTAAGAGTCCCTTTGTTTGGGAAAGTAGCAGAAATGTCGCT 2940
QY 2941 TCTTTCCATGAGTGGAAATGTGGCTGTCCACTCTCCTCCAGGTTCATTTCACTTT 3000
Db 2941 TCTTTCCATGAGTGGAAATGTGGCTGTCCACTCTCCTCCAGGTTCATTTCACTTT 3000
QY 3001 CTTTCCAAACTTATTAACCTCCCTAATCCTGAGACTTTGGAAAGGTGGAGGAGAAC 3060
Db 3001 CTTTCCAAACTTATTAACCTCCCTAATCCTGAGACTTTGGAAAGGTGGAGGAGAAC 3060

Db 3001 CTTTCCAAACTTATTAACCTCCCTAATCCTGAGACTTTGGAAAGGTGGAGGAGAAC 3060
QY 3061 TGTGCTTATCTCCCTCCCTCCCTGATGTGTCAACATTTGATGTCAATTTACTAATC 3120
Db 3061 TGTGCTTATCTCCCTCCCTCCCTGATGTGTCAACATTTGATGTCAATTTACTAAT 3120
QY 3121 TACATTCAGTGGCTGTACAAATACAGCTGTGTAGTAAGAGAGATTCRSGATGCTAGAG 3180
Db 3121 TACATTCAGTGGCTGTACAAATACAGCTGTGTAGTAAGAGAGATTCRSGATGCTAGAG 3180
QY 3181 GAATATTTGGGTTCATTTACATGTACACTACATAGCAAGTTGATACTCATGTTCATGTT 3240
Db 3181 GAATATTTGGGTTCATTTACATGTACACTACATAGCAAGTTGATACTCATGTTCATGTT 3240
QY 3241 TTTTAAATTTAGTGAATTTGTGTCTTAAAGTCTTAACTTCCATACTTCAATCATGTATG 3300
Db 3241 TTTTAAATTTAGTGAATTTGTGTCTTAAAGTCTTAACTTCCATACTTCAATCATGTATG 3300
QY 3301 AACTTCCATGTTTCTTCTGATAAATGGAATGTAGGTTCACTGCCACTTCATGAGATAT 3360
Db 3301 AACTTCCATGTTTCTTCTGATAAATGGAATGTAGGTTCACTGCCACTTCATGAGATAT 3360
QY 3361 CTCTGCTACGCTTCCAAAGTTGTTCTCAATGACATTAAGCAAGTTGGGTTTCCCAATCA 3420
Db 3361 CTCTGCTACGCTTCCAAAGTTGTTCTCAATGACATTAAGCAAGTTGGGTTTCCCAATCA 3420
QY 3421 TCCCTTAGGCTAGTAAATCTTGTGTGTTCCCTGCTGTCTCCGTATTAAGTGACCGGC 3480
Db 3421 TCCCTTAGGCTAGTAAATCTTGTGTGTTCCCTGCTGTCTCCGTATTAAGTGACCGGC 3480
QY 3481 AAATAAATCTCATAGCAGTTAAATAAAAACATCTTTGGAGGATGGAGAGACAGAGAGG 3540
Db 3481 AAATAAATCTCATAGCAGTTAAATAAAAACATCTTTGGAGGATGGAGAGACAGAGAGG 3540
QY 3541 AGATGGGAACAAAATAGAGATTTCTTAAGATTTTGTAAACCAATGTTTCATGTAG 3600
Db 3541 AGATGGGAACAAAATAGAGATTTCTTAAGATTTTGTAAACCAATGTTTCATGTAG 3600
QY 3601 AATGCAAAATGTTGGCAGCTCAAAATATGAATGTGTAGCAACTGTAGTGTGTCTCAGT 3660
Db 3601 AATGCAAAATGTTGGCAGCTCAAAATATGAATGTGTAGCAACTGTAGTGTGTCTCAGT 3660
QY 3661 TTGTAGTGTAGGAGTGTATTTTCTCTGATCAATATAAATGCTGGAACTACTCAAAA 3720
Db 3661 TTGTAGTGTAGGAGTGTATTTTCTCTGATCAATATAAATGCTGGAACTACTCAAAA 3720
QY 3721 AAAAAAAAAAAAAAAAAAAAAA 3742
Db 3721 AAAAAAAAAAAAAAAAAAAAAA 3742

Search completed: October 21, 2003, 11:11:12
Job time : 727.498 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 765.637 Seconds
(without alignments)
13107.130 Million cell updates/sec

Title: US-09-762-194-7
Perfect score: 3742
Sequence: 1 cagtggtgtgttgtagag.....aaaaaaaaaaaaaaaaaaaaa 3742

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/1/pubpna/ECT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/ECTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
------------	-----------	-------	-------	--------	-------	-------------

1	3251.6	86.9	4937	13	US-10-044-090-76	Sequence 76, Appl
2	894	23.9	910	14	US-10-043-487-47	Sequence 47, Appl
c 3	519.2	13.9	581	14	US-10-106-698-125	Sequence 125, Appl
4	509.2	13.6	656	10	US-09-764-864-757	Sequence 757, Appl
5	449.6	12.0	481	10	US-09-764-864-342	Sequence 342, Appl
6	412	11.0	464	11	US-09-918-995-5569	Sequence 5569, Appl
7	405.4	10.8	490	11	US-09-918-995-5132	Sequence 5132, Appl
c 8	366	9.8	366	10	US-09-964-844A-352	Sequence 352, Appl
c 9	366	9.8	366	10	US-09-880-107-1238	Sequence 1238, Appl
10	215.8	5.8	444	11	US-09-918-995-12481	Sequence 12481, A
11	212.8	5.7	435	10	US-09-983-965-3690	Sequence 3690, Appl
12	209.6	5.6	1117	13	US-10-027-632-85144	Sequence 85144, A
13	133	3.3	133	10	US-09-998-598-2218	Sequence 2218, Appl
14	117.8	3.1	440	11	US-09-918-995-11578	Sequence 11578, A
15	93.6	2.5	567	9	US-09-925-302-132	Sequence 132, Appl
16	71	1.9	313	10	US-09-983-965-2834	Sequence 2834, Appl
c 17	63.4	1.7	14006	12	US-10-311-455-1931	Sequence 1931, Appl
18	60	1.6	60	12	US-09-908-975-10969	Sequence 10969, A
c 19	56.8	1.5	9539	12	US-10-240-453-54	Sequence 54, Appl
c 20	56.8	1.5	9539	14	US-10-239-676-52	Sequence 52, Appl
c 21	55.6	1.5	6668	12	US-10-311-455-1670	Sequence 1670, Appl
c 22	55.6	1.5	7657	12	US-10-311-455-1995	Sequence 1995, Appl
c 23	55.6	1.5	7657	14	US-10-239-676-185	Sequence 185, Appl
24	54.6	1.5	554	13	US-10-101-467-106	Sequence 106, Appl
25	53.2	1.4	650	13	US-10-027-632-320324	Sequence 320324, Appl
c 26	53.2	1.4	3673778	12	US-10-312-841-2	Sequence 2, Appl
27	52.8	1.4	522	13	US-10-101-487-71	Sequence 71, Appl
c 28	52.8	1.4	530	13	US-10-101-487-73	Sequence 73, Appl
29	52.8	1.4	554	13	US-10-101-487-69	Sequence 69, Appl
c 30	52.6	1.4	6334	12	US-10-311-455-1186	Sequence 1186, Appl
c 31	52.4	1.4	410	12	US-09-814-353-4678	Sequence 4678, Appl
c 32	52.4	1.4	410	12	US-09-814-353-10977	Sequence 10977, A
33	52.2	1.4	1528	13	US-10-027-632-39070	Sequence 39070, A
34	52.2	1.4	1528	13	US-10-027-632-83911	Sequence 83911, A
c 35	52.2	1.4	10369	12	US-10-311-455-365	Sequence 365, Appl
c 36	52	1.4	7571	12	US-10-311-455-500	Sequence 500, Appl
c 37	52	1.4	17934	12	US-10-311-455-1692	Sequence 1692, Appl
c 38	51.8	1.4	6944	14	US-10-172-086-112	Sequence 112, Appl
c 39	51.8	1.4	113515	12	US-10-311-455-2147	Sequence 2147, Appl
c 40	51.6	1.4	529	10	US-09-983-965-2109	Sequence 2109, Appl
c 41	51.6	1.4	11670	12	US-10-240-452-25	Sequence 25, Appl
c 42	51.4	1.4	442	10	US-09-960-352-12911	Sequence 129.1, A
c 43	51.2	1.4	659158	10	US-09-771-208-20	Sequence 20, Appl
44	51	1.4	268	10	US-09-960-352-11467	Sequence 11467, A
45	50.8	1.4	3489	12	US-10-294-804-1	Sequence 1, Appl

Search completed: October 22, 2003, 03:34:47
Job time : 770.637 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 5899.62 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-7
Sequence: 1 cagtgatgtgttcagag.....aaaaaaaaaaaaaaaaaaaaa 3742

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estcom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_nam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rtd:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	
1	1338.8	35.8	3963	11	AK031693	AK031693 Mus muscu	
2	1191.6	31.8	2477	11	AK030510	AK030510 Mus muscu	
c	3	1074.8	28.7	1130	9	AL574093	AL574093 AL574093
4	1051	28.1	3237	11	AK035576	AK035576 Mus muscu	
5	1014.4	27.1	1127	9	AL550130	AL550130 AL550130	
c	6	1005	26.9	1201	9	AL528732	AL528732 AL528732
7	986.4	26.4	1201	9	AL528733	AL528733 AL528733	
c	8	952.4	25.5	1070	13	BX394445	BX394445 BX394445
9	868.8	23.2	1005	13	BQ070423	BQ070423 AGENCOURT	
c	10	847.6	22.7	908	13	BX415760	BX415760 BX415760
11	780.4	20.9	794	10	BG742834	BG742834 602632568	
12	765.4	20.5	835	9	AU119683	AU119683 AU119683	
13	761.8	20.4	845	9	AU131191	AU131191 AU131191	
14	751.4	20.1	990	13	BQ893803	BQ893803 AGENCOURT	
15	740	19.8	830	9	AU138373	AU138373 AU138373	
16	738	19.7	776	12	BM716134	BM716134 UI-E-CKI-	
17	734.8	19.6	920	13	BU172503	BU172503 AGENCOURT	
18	728.2	19.5	1346	11	BC007328	BC007328 Homo sapi	
19	716.6	19.2	867	10	BG676152	BG676152 602622551	
c	20	714	19.1	716	13	BU685931	BU685931 UI-CF-DU1
21	708.6	18.9	785	13	BU940431	BU940431 AGENCOURT	
22	703.6	18.8	785	9	AU134834	AU134834 AU134834	
23	701.6	18.7	782	9	AU141757	AU141757 AU141757	
c	24	696.6	18.6	715	13	BU609177	BU609177 UI-CF-FNO
25	691	18.5	747	9	AU138331	AU138331 AU138331	
26	681.4	18.2	707	10	BG696701	BG696701 602659717	
c	27	681	18.2	690	12	BM665224	BM665224 UI-E-CKI-
28	675	18.0	874	13	BU151347	BU151347 AGENCOURT	
29	672.4	18.0	676	12	BM702509	BM702509 UI-E-CKI-	
c	30	670.4	17.9	684	13	BU686234	BU686234 UI-CF-DU1
31	662.4	17.7	728	10	BF965779	BF965779 60227408	
c	32	661.4	17.7	663	13	BU679690	BU679690 UI-CF-EC1
c	33	660	17.6	660	13	BU733517	BU733517 UI-S-CQ1-
34	657.2	17.6	736	14	CB962566	CB962566 AGENCOURT	
c	35	657	17.6	657	12	BM968524	BM968524 UI-S-CKI-
c	36	653.8	17.5	657	13	BU730180	BU730180 UI-S-CKI-
37	649.6	17.4	836	10	BF340950	BF340950 602038263	
c	38	648.8	17.3	664	12	BM971589	BM971589 UI-S-CKI-
39	643	17.2	668	12	BM687906	BM687906 UI-S-CKI-	
40	642.4	17.2	645	13	BQ549647	BQ549647 1K83106.X	
41	641.8	17.2	828	10	BG432926	BG432926 602495747	
c	42	635.4	17.0	656	12	BM984811	BM984811 UI-C-EC1
43	631.6	16.9	758	10	BG719490	BG719490 602610048	
44	627.4	16.8	945	10	BG033829	BG033829 602301209	
45	626	16.7	778	10	BE895149	BE895149 601436077	

Search completed: October 21, 2003, 21:04:19
Job time : 5911.62 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Computer Ltd.

CM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 3345.39 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-9
Perfect score: 1308
Sequence: 1 atgttgtgtctcccaatt.....ccagcatttcaccagatga 1308

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_em:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_ther:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_man:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1308	100.0	3742	6	AX210037	Sequence
2	1295	99.0	1977	9	AF293357	Homo sapi
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4	1291.8	98.8	1615	6	AX301208	Sequence
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8	1177.4	90.0	5799	6	AX210061	Sequence
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12	1175.8	89.9	1458	6	AX209991	Homo sapi
13	1175.8	89.9	5214	9	HS800681	Sequence
14	1173.4	89.7	1191	6	AX209993	Homo sapi
15	948.2	72.5	1323	10	AX208915	Sequence
16	943.4	72.1	1323	10	AX246699	Rattus no
17	941.8	72.0	1803	10	AF173380	Mus muscu
18	854.6	65.3	3629	10	BC043321	Mus muscu
19	854.6	65.3	5218	10	BC041777	Mus muscu
20	854.6	65.3	5219	10	BC042206	Mus muscu
21	836.6	64.0	1142	9	BC017740	Mus muscu
22	740	56.6	830	6	BD149398	Homo sapi
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25	410.4	31.4	2548	9	AK000172	Homo sapi
26	313	23.9	729	9	AK093875	Homo sapi
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28	252.6	19.3	1229	10	BC030860	Homo sapi
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31	219	16.7	131299	9	AF165145	Homo sapi
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35 218 16.7 700 6 AX210048 Sequence
36 216.4 16.5 186901 2 AF267167 AF267167 Homo sapi
37 215 16.4 215 6 AX210028 Sequence
38 214 16.4 2333 6 AX210036 Sequence
39 205.4 15.7 700 6 AX210050 Sequence
40 201.4 15.4 203 6 AX210030 Sequence
41 191.4 14.6 65493 2 AC099807 Homo sapi
42 178.2 13.6 1003 5 AF176665 AF176665 Homo sapi
43 174.6 13.3 194355 2 AC116511 AF116511 Mus muscu
44 169.8 13.0 270745 2 AC097544 AC097544 Rattus no
45 161.4 12.3 4021 9 AB018317 AB018317 Homo sapi

ALIGNMENTS

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LOCUS AX210037 3742 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 53 from Patent WO0157209.
ACCESSION AX210037
VERSION AX210037.1 GI:15424423
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Nahmias,C., Strosberg,A.D. and Nouet,S.
TITLE Novel family of proteins, called atip, nucleic sequences coding for same and uses thereof
JOURNAL Patent: WO 0157209-A 53 09-AUG-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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Best Local similarity 100.0%; Pred. No. 1.6e-286;

Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     293  ATGTTGTTGCTCCCAAAATCTCCTTATCCACCAATTCACATAGCACTGAGGCGCAAGAA 352

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RESULT 2
AF293357
LOCUS      Homo sapiens AT2 receptor-interacting protein 1 mRNA, complete cds.
DEFINITION
ACCESSION AF293357
VERSION    AF293357.1 GI:117224595
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SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE   1 (bases 1 to 1977)
AUTHORS    Nouet, S. and Nahmias, C.
TITLE      Cloning of human AT2 receptor-interacting protein 1 (ATIP1)
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 1977)
AUTHORS    Nouet, S. and Nahmias, C.
TITLE      Direct Submission
JOURNAL    Submitted (03-AUG-2000) Institut Cochin de Genetique Moleculaire,
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 ACCESSION AF121259.1 GI:11275569
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Seibold,S., Rudloff,C., Weber,M., Galle,J., Warner,C. and Marx,M.
 TITLE Identification of a new tumor suppressor gene located at chromosome
 8p21.3-22
 JOURNAL FASEB J. (2003) In press
 PUBMED 12692079
 REFERENCE
 AUTHORS Seibold,S. and Marx,M.
 TITLE Direct Submission
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 REFERENCE
 AUTHORS Seibold,S. and Marx,M.
 TITLE Direct Submission
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 421 TGTGAGAAATTAGAAAACCGAGGATGAGTTACAAACAGTGTATGAGCAATTCGTCAG 480
 DB
 421 TGTGAGAAATTAGAAAACCGAGGATGAGTTACAAACAGTGTATGAGCAATTCGTCAG 480
 QY
 481 CAGCACCGCTGAAAAACAGACGAGAGATCGGCTTAAGAGTTTACACCCAGGGAG 540
 DB
 481 CAGCACCGCTGAAAAACAGACGAGAGATCGGCTTAAGAGTTTACACCCAGGGAG 540
 QY
 541 TATGAAAAGCTTCGGGACACTTACATTGAAAGAGCAGAGAGTACAAAATGCAATTGCA 600
 DB
 541 TATGAAAAGCTTCGGGACACTTACATTGAAAGAGCAGAGAGTACAAAATGCAATTGCA 600
 QY
 601 GACGAGTTGACACACTTAAA---TGGCGATGAAACCTCTAAGTTGGAATTTGAGCTAGC 657
 DB
 601 GACGAGTTGACACACTTAAAATGCTGGCGATGAAACCTCTAAGTTGGAATTTGAGCTAGC 660
 QY
 658 CACTCAGAGAAACTTGAATTCATAAGAGGCTTATGAGCCTCCCTTCAGAAATTAAG 717
 DB
 661 CACTCAGAGAACTTGAATTCATAAGAGGCTTATGAGCCTCCCTTCAGAAATTAAG 720
 QY
 718 AAGGCCATGAAATAGAAAAGAAATCGCTTGAAGATTTACTTTCTGAGAGCAGGAATCG 777
 DB
 721 AAGGCCATGAAATAGAAAAGAAATCGCTTGAAGATTTACTTTCTGAGAGCAGGAATCG 780
 QY
 778 CTAGAGAGCAATCATGATCTGAGAGAGTGAATGATGCTTTAAATGAAAATTTGAAA 837
 DB
 781 CTAGAGAGCAATCATGATCTGAGAGAGTGAATGATGCTTTAAATGAAAATTTGAAA 840
 QY
 838 TCAGAGAAACAAAAAGAGCAACAGAAAAAGCAAAATTTGAAAATTCCTCAGATCAT 897

D6	841	TGAGAGACCAAAAAGAGACGACGAAAAAGCAAATTTGGAAATCCTCAGATCATG 900
QY	898	TATCTAGACACAGAGATTAGAAAGCCTGAAGCTGTGTTAGAGATCAAGAATGAGAACTG 957
D6	901	TATCTAGACACAGAGATTAGAAAGCCTGAAGCTGTGTTAGAGATCAAGAATGAGAACTG 960
QY	958	CATCACACAGACATCAAGTTCATGAATTCGAGAACTGGTGGAACAACAACAGCATG 1017
D6	961	CATCACACAGACATCAAGTTCATGAATTCGAGAACTGGTGGAACAACAACAGCATG 1020
QY	1018	GTTGCACAAATTTGAAGCTTCCAGCAGAGAAATGAAGATCGAATCGATGGACAG 1077
D6	1021	GTTGCACAAATTTGAAGCTTCCAGCAGAGAAATGAAGATCGAATCGAATGGACAG 1080
QY	1078	CACATGGCAATCTCAAGGACGCTTTCCAGGACGAGCGTGTTCGAGAGTGCCTGGAG 1137
D6	1081	CACATGGCAATCTCAAGGACGCTTTCCAGGACGAGCGTGTTCGAGAGTGCCTGGAG 1140
QY	1138	AAGGATCGAAAGTCACACGAGACTCTCATGCGAAAGCAGAGAGCTTCTGTGGAAC TG 1197
D6	1141	AAGGATCGAAAGTCACACGAGACTCTCATGCGAAAGCAGAGAGCTTCTGTGGAAC TG 1200
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D6	1201	CACAAATGGGACGCTGTGTAGCCCCAACAGATCCCCACATCCTCCGCCATCCCTTCGAG 1260
QY	1258	TCACACAGGAAATCGGGCTCTTCCTTAGCCCCAGCATTCACCCAGATGA 1308
D6	1261	TCCACAGGAAATCGGGCTCTTCCTTAGCCCCAGCATTCACCCAGATGA 1311
RESULT 4		
AX301208		
LOCUS	AX301208	1615 bp DNA linear PAT 30-NOV-2001
DEFINITION	Sequence 50 from Patent W00185942.	
ACCESSION	AX301208	
VERSION	AX301208.1	GI:17382299
KEYWORDS	.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
	1	
	Azu,H., Tang,Y.T., Au-Yang,J., Lu,D.A., Baughn,M.R., Hillman,J.L.,	
	Azmi,Z.Y., Lal,P., Yao,M.G., Bandman,O., Burford,N., Batra,S.,	
	Kearney,L. and Pelicky,J.L.	
TITLE	Cycloketon-associated proteins	
JOURNAL	Patent: WO 0185942-A 50 15-NOV-2001;	
	Incyte Genomics, Inc. (US)	
FEATURES	Location/Qualifiers	
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	/db_xref="taxon:9606"	
	/note="Incyte ID No: 1403289CB1"	
BASE COUNT	540 a 344 c 370 g 361 t	
ORIGIN		

Search completed: October 21, 2003, 17:18:08
Job time : 3348.39 secs

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308	100.0	1308	21	AAZ99092 Human ATIP coding
2	1308	100.0	3742	21	AAZ99091 Human ATIP gene.
3	1308	100.0	3742	22	AAH74362 Nucleotide sequence
4	1291.8	98.8	1615	24	AAZ99905 Polynucleotide enc
5	1177.4	90.0	1758	22	AAH74324 Nucleotide sequence
6	1177.4	90.0	3654	22	AAH74323 Nucleotide sequence
7	1177.4	90.0	3807	25	ABX10230 Human cDNA encod
8	1177.4	90.0	4937	25	ABX63076 Human cDNA #76 di
9	1176.2	89.9	3315	22	AAH19632 Human cDNA sequen
10	1175.8	89.9	1369	22	AAH74322 Nucleotide sequenc
11	1175.8	89.9	1458	22	AAH74325 Nucleotide sequenc
12	1174.2	89.8	5799	22	AAH74383 Nucleotide sequenc
13	1173.4	89.7	1191	22	AAH74326 Nucleotide sequenc
14	1172.6	89.6	5961	22	AAH74385 Nucleotide sequenc
15	941.8	72.0	1323	21	AAZ99089 Mouse ATIP coding
16	941.8	72.0	1803	21	AAZ99088 Mouse ATIP gene.
17	894	68.3	910	24	ABX51467 Human cDNA encodin
18	740	56.6	830	22	AAH07946 Human cDNA clone (
19	678	51.8	775	22	AAH74327 Nucleotide sequenc
20	600.4	45.9	3287	21	AAF22352 Human secreted pro
21	509.2	38.9	656	22	AAZ99090 Human cDNA encodin
22	509.2	38.9	656	25	ABX73919 Human novel polynu
23	457.6	35.0	791	25	AAZ53121 Human genomic DNA
24	449.6	34.4	481	22	AAZ26163 Human cDNA encodin
25	449.6	34.4	481	25	ABX73504 Human novel polynu
26	234.6	17.9	242	25	ABX74609 Human ATIP coding
27	232.4	17.8	354	21	AAZ99090 Mouse ATIP coding
28	219	16.7	2850	22	Nucleotide sequenc
29	218	16.7	700	22	AAH74372 Nucleotide sequenc
30	215	16.4	215	22	AAH74353 Nucleotide sequenc
31	214	16.4	2333	22	AAH74361 Nucleotide sequenc
32	212.8	16.3	435	25	ABX53761 Bovine EST associa
33	205.4	15.7	700	22	AAH74374 Nucleotide sequenc
34	201.4	15.4	203	22	AAH74355 Nucleotide sequenc
35	161.6	12.4	562	23	ABV48083 Human prostate exp
36	161.4	12.3	4184	25	ABX71114 Novel human cDNA s
37	160.4	12.3	338	21	AAA41587 Human secreted exp
38	133	10.2	133	24	ABV88907 Human colon cancer
39	121.4	9.3	900	22	AAH74371 Nucleotide sequenc
40	121.4	9.3	2672	24	ABK09997 cDNA encoding huma
41	121	9.3	413	22	AAH74352 Nucleotide sequenc
42	120	9.2	120	22	AAH74363 Nucleotide sequenc
43	120	9.2	600	22	AAH74378 Nucleotide sequenc
44	117	8.9	117	22	AAH74359 Nucleotide sequenc
45	117	8.9	367	22	AAH74329 Nucleotide sequenc

ALIGNMENTS

RESULT 1	
AAZ99092	AAZ99092 standard; cDNA; 1308 BP.
ID	AAZ99092
XX	AC
XX	AAZ99092;
XX	DT
XX	21-JUN-2000 (first entry)
XX	DE
XX	Human ATIP coding sequence.
XX	KW
XX	Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
XX	two-hybrid screen; signal transduction; human.
XX	KW
XX	OS
XX	Homo sapiens.
XX	FN
XX	FR2782084-A1.
XX	PD
XX	11-FEB-2000.
XX	PF
XX	04-AUG-1998; 98FR-0009997.
XX	PR
XX	04-AUG-1998; 98FR-0009997.
XX	(CNRS) CNRS CENT NAT RECH SCI.
XX	PA
XX	Elbaz N, Nahmias C, Strosberg AD;
XX	PI
XX	WPI; 2000-248410/22.
XX	DR
XX	PT
XX	Nucleic acids coding for angiotensin II receptor AT2 interacting
XX	proteins useful in screening assays for receptor-protein interaction.
XX	PS
XX	Claim 1; Page 40-41; 63pp; French.
XX	CC
XX	This sequence represents the open reading frame (ORF) from the cDNA
XX	encoding a human angiotensin II (AT2) receptor interactive protein
XX	(ATIP; AAY83780). The human gene was isolated using a fragment of the
XX	mouse gene (AAZ99088). Cells transformed with vectors containing the
XX	cDNA, or immobilized proteins encoded by it, can be used to screen for
XX	substances that modulate ATIP-AT2 interaction or substances that interact
XX	with ATIP, especially using yeast two- or three-hybrid techniques. Such
XX	substances may be useful for treating disorders associated with anomalous
XX	AT2 receptor signal transduction.
XX	SQ
XX	Sequence 1308 BP; 460 A; 277 C; 294 G; 277 T; 0 other;
Query Match 100.0%; Score 1308; DB 21; Length 1308;	
Best Local Similarity 100.0%; Pred. No. 1.3e-314;	
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	
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Qy	61 TTGCTTCGAACCTTCGACTTCCTTCAGGGTTAGGAGGACACTGTGTTTCCACACA 120

Db 61 TTGCTTGAAACCTTGACTTCCTTCAGGGTTTAGGAGAGCACTGTGTGTTTCCACA 120
QY 121 GTTGAAGAGCAGCGCAAAAGAACTCTGAAGCTTATGTATCCAGGCCACAGACAGCTCC 180
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QY 161 GATGGCTGGCCCTCGAGAAACACTTGAATGACGCAATATAAAACAATAATGTGAAC 240
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QY 241 CAAGTGGATTTATCTCGAGCTCAAGCACTTCTTGCTGTGTATACCAAGTTTGG 300
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Db 301 GCATTGACATTTGATTACAGCACTGCTGTCTGAGCGGAGGAAGCACTGAAACACAC 360
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Db 421 TGTGAGAAATTAGAAAAGCCAGGAATGAGTTACAAAAGTGTATGAGCACTCGTCCAG 480
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Db 461 CAGCACAGGCTGAAAAAGACAGACAGAGAAATCGGCTTAAAGAGTTTACACACAGGAG 540
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Db 721 GGCATGAAATAGAAAGAAATCCCTTGAAGATTTACTTCTGAGAGCAGGAATCGCTA 780
QY 761 GAGAGCAATCAATGATCTGAAGAGTGAATAATGATGCTTTAAATGAAAATTAAGAA 840
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QY 841 GAAGAACAAAAAGAGCAGAGAGAAAAAGCAAAATTTGAAAAATCCTCAGATCATGTAT 900
Db 841 GAAGAACAAAAAGAGCAGAGAGAAAAAGCAAAATTTGAAAAATCCTCAGATCATGTAT 900
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QY 961 CAACAGACATCAAGTTTAAATGAAATGGAGAACTGGTGGACAAACAACAGCAATTGGT 1020
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RESULT 2

AAZ99091
ID AAZ99091 standard; cDNA; 3742 BP.
XX AC AAZ99091;
XX XX
DT 21-JUN-2000 (first entry)
XX DE Human ATIP gene.
XX KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
KW two-hybrid screen; signal transduction; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 293..1600
FT /*tag= a
FT /product= "human ATIP"
FT /note= "angiotensin II (AT2) receptor interactive
protein"
XX FN FR2782084-AL.
XX PD 11-FEB-2000.
XX PF 04-AUG-1998; 98FR-0009997.
XX PR 04-AUG-1998; 98FR-0009997.
XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX Elbaz N, Nahmias C, Strosberg AD;
 PI WPI: 2000-248410/22.
 DR P-PSDB; AAY63780.
 XX Nucleic acids coding for angiotensin II receptor AT2 interacting
 PT proteins useful in screening assays for receptor-protein interaction -
 XX Claim 1; Fig 4; 63pp; French.
 XX This sequence represents the cDNA encoding a human angiotensin II (AT2)
 CC receptor interactive protein (ATIP). The gene was isolated using a
 CC fragment of the mouse gene (AA299088). Cells transformed with vectors
 CC containing the cDNA, or immobilized proteins encoded by it, can be used
 CC to screen for substances that modulate ATIP-AT2 interaction or
 CC substances that interact with ATIP, especially using yeast two- or
 CC three-hybrid techniques. Such substances may be useful for treating
 CC disorders associated with anomalous AT2 receptor signal transduction.
 XX Sequence 3742 BP; 1180 A; 762 C; 793 G; 1007 T; 0 other;
 SQ

Query Match 100.0%; Score 1308; DB 21; Length 3742;
 Best Local Similarity 100.0%; Pred. No. 1.3e-314; Indels 0; Gaps 0;
 Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGTCTCCCAAAATTCCTTATCCACCATTCACATACGACTGACGGCCAAAGGA 60
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 QY 121 GTTGAAGAAGCAGCAAGCAAAAGAAATCCTCGAAGCTTATGTATCCAGCCACAGACAGCTCC 180
 DB 413 GTTGAAGAAGCAGCAAGCAAAAGAAATCCTCGAAGCTTATGTATCCAGCCACAGACAGCTCC 472
 QY 181 GATGCGCTGCCCCCTGAGAAACACTTGGAATTGAGCGAATATATAACAAATGTGAAAC 240
 DB 473 GATGCGCTGCCCCCTGAGAAACACTTGGAATTGAGCGAATATATAACAAATGTGAAAC 532
 QY 241 CAAAGTGGAAATATCCTGCAAGCTCAAGCAGCTTCTGCTGTGCTAATACCAAGTTGAG 300
 DB 533 CAAAGTGGAAATATCCTGCAAGCTCAAGCAGCTTCTGCTGTGCTAATACCAAGTTGAG 592
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 DB 593 GCATTGACAGTTGTGATTCAACCACTCTGCTGAGCGGGAGGAGCACTGAAACAACAC 652
 QY 361 AAAACCCCTATCTCAAGACTTGTTAACCTCCGGGGAGAGCTAGTCACTGTGCTCAACACC 420
 DB 653 AAAACCCCTATCTCAAGACTTGTTAACCTCCGGGGAGAGCTAGTCACTGTGCTCAACACC 712
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 DB 713 TGTGAGAAATTAGAAAAGCCAGGAATGAGTTACAAACAGTGTATGAGCANTTCGTCCAG 772

QY 481 CAGCACCAAGCTGAAAAACAGACGAGAGAGATCGGCTTAAAGAGTTTACACACAGGAG 540
 DB 773 CAGCACCAAGCTGAAAAACAGACGAGAGAGATCGGCTTAAAGAGTTTACACACAGGAG 832
 QY 541 TATGAAAAGCTTCGGGACACTTACATTGAAAGAGCAGAGAGTACAAATGCATTCGAA 600
 DB 833 TATGAAAAGCTTCGGGACACTTACATTGAAAGAGCAGAGAGTACAAATGCATTCGAA 892
 QY 601 GAGCAGTTGACAACTTAAATCGCATGAAACCTCTAAGTTGGAAATGAAAGCTAGCCT 660
 DB 893 GAGCAGTTGACAACTTAAATCGCATGAAACCTCTAAGTTGGAAATGAAAGCTAGCCT 952
 QY 661 TCAGAGAAACTTGAAATGCTTAAAGAGGCTTATGAGCCTCCCTTCAGAAATTAAGAA 720
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 QY 901 CTAGAACAGGAGTTAGAAAGCCTGAAAGCTGTGTTAGAGATCAAGATGAGAACTGCAT 960
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 DB 1373 ATGGCAATCTCAAGCAGCTTCCAGCAGGAGCTGTTCTGCAAGAGTCCGTTGGAGAG 1432
 QY 1141 GAGTGGAAAGTCAACAGCGACTCTCTATGGAACACGAGAGCTCTGTGGAAACTGCAC 1200
 DB 1433 GAGTGGAAAGTCAACAGCGACTCTCTATGGAACACGAGAGCTCTGTGGAAACTGCAC 1492
 QY 1201 AATGGGAGCTGTGTAGCCCAAGAGATCCCAACATCTCTCCGCAATCCCTTTGAGTCA 1260
 DB 1493 AATGGGAGCTGTGTAGCCCAAGAGATCCCAACATCTCTCCGCAATCCCTTTGAGTCA 1552
 QY 1261 CCAGGAAATTCGGGCTCCTTCCCTAAGCCCAAGCATTTCCACCCAGATGA 1308
 DB 1553 CCAGGAAATTCGGGCTCCTTCCCTAAGCCCAAGCATTTCCACCCAGATGA 1600

[illegible]

QY 841 GAAGACAAAAAGAGAGCAAGAGAAAAAGCAAAATTTGAAAAATCTTCAGATCATGTAT 900
|||||
Db 1133 GAAGACAAAAAGAGAGCAAGAGAAAAAGCAAAATTTGAAAAATCTTCAGATCATGTAT 1192
|||||
QY 901 CTAGAACAGAGCTAGAAAGCTTGAAGCTGTGTAGAGATCAAGATGAGAACTGCAT 960
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Db 1193 CTAGAACAGAGCTAGAAAGCTTGAAGCTGTGTAGAGATCAAGATGAGAACTGCAT 1252
|||||
QY 961 CAACAGGACATCAAGTTAATGAAATGGAAACTGGTGAACAACAACAGCAATGGTT 1020
|||||
Db 1253 CAACAGGACATCAAGTTAATGAAATGGAAACTGGTGAACAACAACAGCAATGGTT 1312
|||||
QY 1021 GACAAATTGAAGCGTTTCCAGCGAGGAGATGAAGAATTGAAAGCTGGATGGACAAGCAC 1080
|||||
Db 1313 GACAAATTGAAGCGTTTCCAGCGAGGAGATGAAGAATTGAAAGCTGGATGGACAAGCAC 1372
|||||
QY 1081 ATGGCAATCTCAAGCGAGCTTCCACGGGCGAGCTGTCTGCAAGTCCCTGGAGAG 1140
|||||
Db 1373 ATGGCAATCTCAAGCGAGCTTCCACGGGCGAGCTGTCTGCAAGTCCCTGGAGAG 1432
|||||
QY 1141 GAGTCSAAAGTCAACAAGCGACTCTCTATGAAAAACGAGGAGCTTCTGTGAAACTGCAC 1200
|||||
Db 1433 GAGTCSAAAGTCAACAAGCGACTCTCTATGAAAAACGAGGAGCTTCTGTGAAACTGCAC 1492
|||||
QY 1201 AATGGGACCTGTGTAGCCCGCAAGATCCCCACATCTCCGCCATCCCTTTGGAGTCA 1260
|||||
Db 1493 AATGGGACCTGTGTAGCCCGCAAGATCCCCACATCTCCGCCATCCCTTTGGAGTCA 1552
|||||
QY 1261 CAAAGGAATTCGGGCTCCTTCCCTAGCCCGCAGCATTTCAACCAGATGA 1308
|||||
Db 1553 CAAAGGAATTCGGGCTCCTTCCCTAGCCCGCAGCATTTCAACCAGATGA 1600
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RESULT 4
AAS99905
ID AAS99905 standard; cDNA; 1615 BP.
XX
AC AAS99905;
XX
DT 12-MAR-2002 (first entry)
DE
DE Polynucleotide encoding human cytoskeleton-associated protein #16.
XX
KW Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder; ss;
KW cell proliferative disorder; inflammatory disorder; prion disease;
KW vesicle trafficking disorder; gastrointestinal disorder; muscle disease;
KW neurological disorder; cell motility disorder; reproductive disorder;
KW spinal cord disease; central nervous system disorder; mental disorder;
KW gene therapy; cancer.
XX
OS Homo sapiens.
XX
FN W0200185942-A2.
XX
PD 15-NOV-2001.
XX
XX
PF 03-MAY-2001; 2001WO-US14355.

XX 05-MAY-2000; 2000US-201960P.
PR 08-MAY-2000; 2000US-20729P.
PR 05-JUN-2000; 2000US-209705P.
PR 07-JUN-2000; 2000US-210149P.
PR 21-JUN-2000; 2000US-213215P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Tang YT, Au-Young J, Lu DAM, Baughn MS, Hillman JL;
PI Azimzai Y, Ial P, Yao MG, Bandman O, Burford N, Batra S;
PI Kearney L, Policky JL;
XX
DR WPI; 2002-062248/08.
DR P-PSDB; AAU74345.
XX
XX New cytoskeleton-associated proteins and polynucleotides, useful for
PT diagnosing, preventing and treating cell proliferative, autoimmune,
PT inflammatory, neurological, cell motility, reproductive and muscle
PT disorders -
XX
PS Claim 5; Page 180; 194pp; English.
XX
CC The invention relates to human cytoskeleton-associated polypeptides
CC (CYSKP) and their associated polynucleotide sequences. The sequences are
CC useful in the treatment of disorders associated with overexpression or
CC underexpression of CYSKP in a patient. The disorders include cell
CC proliferative disorders (such as cancer, actinic keratosis,
CC arteriosclerosis, cirrhosis, hepatitis and psoriasis),
CC autoimmune/inflammatory disorders (such as, asthma, atherosclerosis,
CC osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus
CC and anaemia), vesicle trafficking disorders (such as
CC hypercholesterolaemia, diabetes insipidus, Gravel's disease and goitre),
CC gastrointestinal disorders, prion diseases, neurological disorders (such
CC as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease,
CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis
CC and other motor neuron disorders), cell motility disorders, reproductive
CC disorders (such as endometriosis and polycystic ovary syndrome), muscle
CC disorders (such as myocardiitis, migraine, hypertension, hypoglycaemia,
CC myocardial infarction, epilepsy and muscular dystrophy), spinal cord
CC diseases, central nervous system disorders (such as Down syndrome and
CC cerebral palsy) and mental disorders (such as anxiety and schizophrenia).
CC Sequences AAS99890-AAS99923 represent cDNA molecules encoding human
XX CYSKP of the invention.
SQ Sequence 1615 BP; 540 A; 344 C; 370 G; 361 T; 0 other;
Query Match 96.8%; Score 1291.8; DB 24; Length 1615;
Best Local Similarity 99.6%; Pred. No. 1.2e-310;
Matches 1306; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 1 ATGTTGTTGCTCCCAAAATCTCTTATCCACCATTCACATACGACTGAGCGCAAGG 60
|||||
Db 284 ATGTTGTTGCTCCCAAAATCTCTTATCCACCATTCACATACGACTGAGCGCAAGG 343
|||||
QY 61 TTCTTGGAAACCTTCGACTTCCTTCAGGGTTTAGGAGAGCACTGTGTTTCCAGCA 120
|||||

Db 344 TTGCTTCGAAACCTTCGACTTCCTTCAGSGTTTAGGAGAGCACTGTGTGTTTCCACA 403
QY 121 GTTGAAGAAGCAGCGCAAAAGAAATCCTCGAAGCTTATGTATTCAGGCCACAGACAGCTCC 180
Db 404 GTTGAAGAAGCAGCGCAAAAGAAATCCTCGAAGCTTATGTATTCAGGCCACAGACAGCTCC 463
QY 181 GATGGCTGCCCCCTGAGAAAGACCTTGAATTGACGCAATATAAAACAAAATGTGAAC 240
Db 464 GATGGCTGCCCCCTGAGAAACACCTTGAATTGACGCAATATAAAACAAAATGTGAAC 523
QY 241 CAAAAGTGGATTTATCCTCGAGCTCAAGCAGCTTCCTGCTGTGTATACCAAGTTGAG 300
Db 524 CAAAGTGGATTTATCCTCGAGCTCAAGCAGCTTCCTGCTGTGTATACCAAGTTGAG 583
QY 301 GCAATTGACAGTTGTGATTCAACAACCTGCTGTGAGCGGGAGGAGCACTGAAACAAC 360
Db 584 GCAATTGACAGTTGTGATTCAACAACCTGCTGTGAGCGGGAGGAGCACTGAAACAAC 643
QY 361 AAAACCTATCTCAAGACCTGTTAACTTCGGGGAGAGCTAGTCACTGCTTCAACACC 420
Db 644 AAAACCTATCTCAAGACCTGTTAACTTCGGGGAGAGCTAGTCACTGCTTCAACACC 703
QY 421 TGTGAGAAATTAGAAAAGCCAGGAATGAGTTACAAAACAGTGTATGAGCAATCGTCCAG 483
Db 704 TGTGAGAAATTAGAAAAGCCAGGAATGAGTTACAAAACAGTGTATGAGCAATCGTCCAG 763
QY 481 CAGCACCAAGCTGAAAAACAGACAGAGAAATCGGCTTTAAAGAGTTTACACCCAGGAG 540
Db 764 CAGCACCAAGCTGAAAAACAGACAGAGAAATCGGCTTTAAAGAGTTTACACCCAGGAG 823
QY 541 TATGAAAAGCTTCGGGACACTTACATTTGAAGAGCAGAGAGTACAAAATGCAATTCGA 600
Db 824 TATGAAAAGCTTCGGGACACTTACATTTGAAGAGCAGAGAGTACAAAATGCAATTCGA 883
QY 601 GAGCAGTTTGACAACTTAAAT---TGCGCATGAAACCTCTAAGTTGAAATGAAAGTAGC 657
Db 884 GAGCAGTTTGACAACTTAAATGCTGCGCATGAAACCTCTAAGTTGAAATGAAAGTAGC 943
QY 658 CACTCAGAGAACTTGAAATGCTTAAAGAGGCTATGAGCCTCCCTTTCAGAAATTAAG 717
Db 944 CACTCAGAGAACTTGAAATGCTTAAAGAGGCTATGAGCCTCCCTTTCAGAAATTAAG 1003
QY 718 AAAGGCCATGAAATAGAAAAGAAATCGCTTGAAGATTTACTTTCTGAGAGCAGGAATCG 777
Db 1004 AAAGGCCATGAAATAGAAAAGAAATCGCTTGAAGATTTACTTTCTGAGAGCAGGAATCG 1063
QY 778 CTAGAGAGCAAAATCAATGATCTGAAGAGTGAAGATGATGCTTTAAATGAAAATGAAA 837
Db 1064 CTAGAGAGCAAAATCAATGATCTGAAGAGTGAAGATGATGCTTTAAATGAAAATGAAA 1123
QY 838 TCAGAGAGCAAAATGAAAGAGCAAGAGAAAAGCAAAATTTGAAAATTCCTCAGATCATG 897
Db 1124 TCAGAGAGCAAAATGAAAGAGCAAGAGAAAAGCAAAATTTGAAAATTCCTCAGATCATG 1183
QY 898 TATCTAGACAGAGGTTAGAAAAGCTGAAAAGCTGTGTAGAGATCAAGATGAGAAACTG 957
Db 1184 TATCTAGACAGAGGTTAGAAAAGCTGAAAAGCTGTGTAGAGATCAAGATGAGAAACTG 1243

QY 958 CATCAACAGACATCAAGTTAAATGAAATGAGAAACTGSGGACACACACACAGATTCG 1017
Db 1244 CATCAACAGACATCAAGTTAAATGAAATGAGAAACTGSGGACACACACACAGATTCG 1303
QY 1018 GTTGACAAAATTGAAGCGTTTCCAGCAGAGAAATGAAGAATTGAAGCTCGGATGGACAG 1077
Db 1304 GTTGACAAAATTGAAGCGTTTCCAGCAGAGAAATGAAGAATTGAAGCTCGGATGGACAG 1363
QY 1078 CCAATGGCAATCTCAAGCAGCTTTCCACGAGCAGGCTGTCTGCAAGAGTGGTGGAG 1137
Db 1364 CCAATGGCAATCTCAAGCAGCTTTCCACGAGCAGGCTGTCTGCAAGAGTGGTGGAG 1423
QY 1138 AAGAGTTCGAAAGTCAACAAGCGACTCTATGGAACAGAGAGCTTCTGTGGAACCTG 1197
Db 1424 AAGAGTTCGAAAGTCAACAAGCGACTCTATGGAACAGAGAGCTTCTGTGGAACCTG 1483
QY 1198 CCAATGGGAGCCTGTGTAGCCCCAAGAGATCCCCACATCCTCCGCCATCCCTTTGCAG 1257
Db 1484 CCAATGGGAGCCTGTGTAGCCCCAAGAGATCCCCACATCCTCCGCCATCCCTTTGCAG 1543
QY 1258 TCACCAAGCAATTCGGGCTCCCTCCCTAGCCCCCAGCAATTTACCCAGATGA 1308
Db 1544 TCACCAAGCAATTCGGGCTCCCTCCCTAGCCCCCAGCAATTTACCCAGATGA 1594

Search completed: October 22, 2003, 03:34:50
Job time : 270.625 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 2062.19 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-9
Perfect score: 1308
Sequence: 1 atgttgttctcccaatt.....ccagcattccaccagatga 1308

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562794

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_estl:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	943.4	72.1	2477	11 AK030510	AK030510 Mus muscu
2	927.4	70.9	3963	11 AK031693	AK031693 Mus muscu
3	819.4	62.6	1005	13 B0070423	B0070423 AGENCOURT
4	740	56.6	830	9 AUI38373	AUI38373 AUI38373
5	728.2	55.7	1346	11 BC007328	BC007328 Homo sapi
6	692.6	53.0	3237	11 AK035576	AK035576 Mus muscu
7	675.2	51.6	782	9 AUI141757	AUI141757 AUI141757
8	631.6	48.3	758	10 BG719490	BG719490 602690048
9	626	47.9	778	10 BE895149	BE895149 601436077
10	622.6	47.6	950	13 BQ921402	BQ921402 AGENCOURT
11	618.4	47.3	945	10 BQ033829	BQ033829 602301209
12	608.4	46.3	626	12 BK737916	BK737916 K-EST0001
13	600.4	45.9	650	12 BM983699	BM983699 UI-CF-DUI
14	580	44.3	600	12 BM311947	BM311947 ig64c02.y
15	541.4	41.4	645	13 BQ549647	BQ549647 ik99f06.x
16	539.4	41.2	557	10 BE552421	BE552421 hw26b02.x
17	504	38.5	889	10 BF574166	BF574166 602131321
18	484.8	37.1	990	13 BQ893803	BQ893803 AGENCOURT
19	479.4	36.7	495	9 AA702088	AA702088 zif90f09.s
20	479.4	36.7	495	9 AA723012	AA723012 zh30e09.s
21	473.8	36.2	845	9 AUI31191	AUI31191 AUI31191
22	471.4	36.0	510	9 AAI94721	AAI94721 rz32b12.s
23	467.2	35.7	486	9 AA778812	AA778812 zj38a04.s
24	467	35.7	582	10 BG573578	BG573578 602595386
25	455.6	34.8	490	12 BQ011508	BQ011508 UI-1-BC1p
26	451.2	34.5	920	13 BU523654	BU523654 AGENCOURT
27	443.4	33.9	461	9 A1564089	A1564089 tn57b04.x
28	430.6	32.9	748	10 BF141309	BF141309 601769830
29	424.2	32.4	836	10 BF340950	BF340950 602038263
30	420.8	32.2	734	14 CB316595	CB316595 AGENCOURT
31	416.8	31.9	541	4 BX512030	BX512030 RZPD MUs
32	414	31.7	430	9 A1149364	A1149364 gc82c04.x
33	410.6	31.4	454	10 AW984317	AW984317 PM3-HK001
34	410.6	31.4	776	13 BU387252	BU387252 603856971
35	410	31.3	426	9 A1626069	A1626069 ar87f04.x
36	407.6	31.2	600	13 BU921755	BU921755 6093-85 M
37	396.4	30.3	422	10 BF515637	BF515637 UI-H-BW1-
38	395	30.2	440	14 CB128270	CB128270 K-EST0177
39	388.4	29.7	624	12 BM951991	BM951991 UI-M-EH0-
40	387	29.6	507	9 A1363967	A1363967 qk34e08.x
41	386.4	29.5	657	10 BB628131	BB628131 BB628131
42	385.8	29.5	405	9 A1879905	A1879905 ar99c-9.x
43	384.8	29.4	862	13 BU248050	BU248050 6037p1419
44	379.6	29.0	782	13 BU702398	BU702398 UI-M-F10-
45	378.4	28.9	820	13 BU344537	BU344537 6035-2603

CM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 84.402 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-11
Perfect score: 33
Sequence: 1 cgcgatccacagacagaccggaactggag 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_on:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_man:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	72.7	1323	10	AY246699	Mus muscu
2	24	72.7	1803	10	AF173360	Mus muscu
3	24	72.7	3629	10	BC043321	Mus muscu
4	24	72.7	5218	10	BC041777	Mus muscu
5	24	72.7	5219	10	BC042206	Mus muscu
6	24	72.7	194355	2	AC116511	Mus muscu
7	21.4	64.8	1920	6	AX139914	Sequence
8	21.4	64.8	1920	6	BD013824	Promoter
9	21.4	64.8	5800	1	ILZ97015	Lactococcus
10	21.4	64.8	9840	6	AX139909	Sequence
11	21.4	64.8	9840	6	BD013820	Promoter
12	21.4	64.8	205187	2	AC137156	Mus muscu
13	21.4	64.8	223132	10	AC123870	Mus muscu
14	21.4	64.8	251396	2	AC128362	Mus muscu
15	21.4	64.8	254304	2	AC133760	Rattus no
16	21.2	64.2	307349	2	AC115785	Mus muscu
17	21	63.6	242130	2	AC108556	Mus muscu
18	20.8	63.0	1323	10	AY208915	Rattus no
19	20.8	63.0	130665	10	AF289666	Mus muscu
20	20.8	63.0	166045	2	AC134957	Tetraodon
21	20.8	63.0	201605	10	AF289667	Mus muscu
22	20.8	63.0	205602	10	AF325177	Mus muscu
23	20.8	63.0	263706	2	AC097149	Rattus no
24	20.8	63.0	270745	2	AC097544	Rattus no
25	20.6	62.4	2879	1	AB027515	Erythroba
26	20.6	62.4	70751	2	AC101724	Mus muscu
27	20.6	62.4	232976	2	AC116557	Mus muscu
28	20.6	62.4	301276	1	AE016758	Escherich
29	20.4	61.8	1496	5	AY219410	Salvelinu
30	20.4	61.8	9698	1	AE012025	Xanthomon
31	20.4	61.8	127376	2	AC141672	Apis mell
32	20.4	61.8	220998	2	AC102965	Rattus no
33	20.4	61.8	226193	2	AC120679	Rattus no

c 34 20.4 61.8 242366 2 AC121386
 c 35 20.4 61.8 244696 2 AC103554
 c 36 20.2 3068 6 E09269
 c 37 20.2 3068 6 E12118
 c 38 20.2 3068 6 I15249
 c 39 20.2 3068 6 I62883
 c 40 20.2 61.2 66658 2 AC110649_3
 c 41 20.2 61.2 110000 2 AC110649_2
 c 42 20.2 229635 2 AC094256
 c 43 20.2 61.2 253729 2 AC094816
 c 44 20.2 61.2 256344 2 AC127789
 c 45 20.2 61.2 269267 2 AC110861

Search completed: October 21, 2003, 17:18:12
 Job time : 88.402 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:18 ; Search time 6.34512 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-11
Perfect score: 33
Sequence: 1 cgcgataccagacagaccgcgacgaactggag 33

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 19Jun03.*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	33	100.0	33	21	AAZ99094
2	24	72.7	354	21	AAZ99090
3	24	72.7	1323	21	AAZ99089
4	24	72.7	1803	21	AAZ99088
5	21.4	64.8	9840	22	AAZ99087
6	20.2	61.2	3068	14	AAQ43721
7	20.2	61.2	3068	17	AAQ43721
8	20	60.6	852	23	AAI16666
9	20	60.6	879	21	AAI16666
10	20	60.6	1035	21	AAI16666
11	19.4	58.8	275	24	AAQ43731
12	19	57.6	2255	23	ABL21890
13	19	57.6	47066	23	ABL21890
14	18.8	57.0	694	22	AAI16666
15	18.8	57.0	659158	25	AAI16666
16	18.6	56.4	560	22	AAI10243
17	18.6	56.4	2219	22	AAI17456
18	18.6	56.4	169998	24	AAI36511
19	18.6	56.4	197496	24	ABN85384
20	18.4	55.8	1398	23	ABL29997
21	18.4	55.8	3629	23	ABL29996
22	18.4	55.8	8605	22	AAI161181
23	18.4	55.8	9408	19	AAV68396
24	18.2	55.2	240	25	ABZ19291
25	18.2	55.2	283	25	ABZ20035
26	18.2	55.2	392	21	AAQ09149
27	18.2	55.2	563	24	ABQ60913
28	18.2	55.2	625	25	ABZ36677
29	18.2	55.2	640	25	ABZ36557
30	18.2	55.2	867	24	ABN98803
31	18.2	55.2	1200	21	AAQ33758
32	18.2	55.2	1424	22	AAI193599
33	18.2	55.2	1447	21	AAQ77496
34	18.2	55.2	2680	23	ABL18449
35	18.2	55.2	3150	23	ABL21324
36	18.2	55.2	4502	22	AAQ72445
37	18.2	55.2	6130	23	ABL18448
38	18.2	55.2	9475	22	AAQ72443
39	18.2	55.2	201143	24	ABK83568
40	18	54.5	4013	22	AAQ67437
41	18	54.5	39328	24	ABU91800
42	18	54.5	4403765	22	AAI199683
43	18	54.5	4411529	22	AAI199682
44	17.8	53.9	362	21	AAQ09806
45	17.8	53.9	381	21	AAQ03400

ALIGNMENTS

RESULT 1
AAZ99094

XX
AC AAZ99094;

XX
DE Mouse ATIP gene primer oligo.sens.

XX
OS Mus sp.

XX
PD 11-FEB-2000.

04-AUG-1998: 98ER-0009997

XX
RI

(NAME / SURNAME) NAME SURNAME

Elbez N Nabias C Stroosborgh

BT
XX
077 / 01604Z-0007 / TFM

XX
XX

Sequence 33 BP: 9 A: 10 C: 12 G: 2 T: 0 other: 0

Query Match 100.0%; Score 33; DB 21; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

db
1 CGCGGATCCCAGACAGACCGGACCGAACTGGAG 33

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 6.75201 Seconds
(without alignments)
13107.130 Million cell updates/sec

Title: US-09-762-194-11

Perfect score: 33
Sequence: 1 cggatccagacagaccggaactggag 33

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

1	19.4	58.8	275	9	US-09-728-446-581	Sequence 581, App
2	19.2	58.2	263	13	US-10-027-632-143193	Sequence 143193, App
c 3	19.2	58.2	581	13	US-10-027-632-134093	Sequence 134093, App
c 4	19.2	58.2	581	13	US-10-027-632-134094	Sequence 134094, App
5	19.2	58.2	640	13	US-10-027-632-143192	Sequence 143192, App
6	19.2	58.2	820	13	US-10-027-632-143189	Sequence 143189, App
7	19.2	58.2	820	13	US-10-027-632-143191	Sequence 143191, App
c 8	19.2	58.2	854	13	US-10-027-632-173748	Sequence 173748, App
c 9	19.2	58.2	897	14	US-10-156-761-357	Sequence 357, App
c 10	19.2	58.2	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 11	18.8	57.0	587	12	US-10-029-386-4316	Sequence 4316, Ap
c 12	18.8	57.0	659158	10	US-09-771-208-20	Sequence 20, Appl
c 13	18.6	56.4	197496	10	US-09-877-177-10	Sequence 10, Appl
c 14	18.4	55.8	573	14	US-10-156-761-7365	Sequence 7365, Ap
15	18.4	55.8	3071	13	US-10-156-761-7365	Sequence 14585, Ap
c 16	18.4	55.8	715517	13	US-10-027-632-114585	Sequence 53716, A
17	18.2	55.2	474	11	US-09-918-995-21180	Sequence 21180, A
18	18.2	55.2	480	11	US-09-918-995-13907	Sequence 13907, A
c 19	18.2	55.2	867	9	US-09-770-445-571	Sequence 571, App
c 20	18.2	55.2	888	14	US-10-156-761-2936	Sequence 2936, Ap
c 21	18.2	55.2	1416	14	US-10-156-761-4207	Sequence 4207, Ap
c 22	18.2	55.2	2322	12	US-09-814-353-19200	Sequence 19200, A
c 23	18.2	55.2	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 24	18	54.5	514	13	US-10-027-632-46468	Sequence 46468, A
c 25	18	54.5	599	13	US-10-027-632-67722	Sequence 67722, A
c 26	18	54.5	599	13	US-10-027-632-67747	Sequence 67747, A
c 27	18	54.5	599	13	US-10-027-632-295388	Sequence 295388, A
c 28	17.8	53.9	428	11	US-09-918-995-1571	Sequence 1571, Ap
c 29	17.8	53.9	860	13	US-10-027-632-120951	Sequence 120951, Ap
c 30	17.8	53.9	860	13	US-10-027-632-120952	Sequence 120952, Ap
c 31	17.8	53.9	860	13	US-10-027-632-120953	Sequence 120953, Ap
c 32	17.8	53.9	1800	14	US-10-156-761-856	Sequence 856, App
c 33	17.8	53.9	1875	14	US-10-156-761-7458	Sequence 7458, App
c 34	17.8	53.9	2085	14	US-10-156-761-6252	Sequence 6252, Ap
c 35	17.8	53.9	2358	14	US-10-043-467-59	Sequence 59, Appl
c 36	17.8	53.9	2797	14	US-10-060-036-46	Sequence 46, Appl
37	17.8	53.9	11962	10	US-09-905-129-20	Sequence 20, Appl
38	17.8	53.9	11962	10	US-09-991-630-20	Sequence 20, Appl
39	17.8	53.9	11967	10	US-09-905-129-3	Sequence 3, Appli
40	17.8	53.9	11967	10	US-09-991-630-3	Sequence 3, Appli
c 41	17.8	53.9	14646	12	US-09-873-319-691	Sequence 691, App
c 42	17.8	53.9	14646	12	US-09-960-706-1043	Sequence 1043, Ap
43	17.6	53.3	157	12	US-10-029-386-18917	Sequence 18917, A
c 44	17.6	53.3	292	11	US-09-968-433-56	Sequence 56, Appl
45	17.6	53.3	535	12	US-10-029-386-5161	Sequence 5161, Ap

Search completed: October 22, 2003, 04:13:27
Job time : 2323.75 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 52.0277 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-11
Perfect score: 33
Sequence: 1 cgcggatccacagacagcggaggaactggag 33
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_in:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	72.7	352	13	BY068750
2	24	72.7	358	9	AI466472
3	24	72.7	364	13	BY130313
4	24	72.7	380	10	BE449013
5	24	72.7	487	10	BF535672
6	24	72.7	500	9	AA880300
7	24	72.7	517	10	BE632532
8	24	72.7	560	14	CD565243
9	24	72.7	624	12	BM951991
10	24	72.7	657	10	BB628131
11	24	72.7	670	10	BB636465
12	24	72.7	710	14	CE723104
13	24	72.7	782	13	BU702398
14	24	72.7	950	13	BQ921402
15	24	72.7	2477	11	AK030510
16	24	72.7	3237	11	AK035576
17	24	72.7	3963	11	AK031693
18	23	69.7	530	13	BQ830956
19	22.4	67.9	732	14	CE246442
20	22.2	67.3	1201	13	EX334102
21	21.4	64.8	688	28	BH969640
22	21.4	64.8	701	10	BF468054
23	21.4	64.8	954	14	CE203504
24	21.2	64.2	908	10	BG107884
25	21	63.6	368	12	BI975959
26	21	63.6	1083	29	CNS055MO
27	20.8	63.0	376	14	CE691075
28	20.8	63.0	560	12	B2217670
29	20.8	63.0	809	10	BF973404
30	20.8	63.0	875	10	BE410275
31	20.6	62.4	417	13	BY458150
32	20.6	62.4	462	10	BF951635
33	20.6	62.4	896	14	CD360742
34	20.4	61.8	131	26	BH712463
35	20.4	61.8	299	28	BH604194
36	20.4	61.8	348	28	BH459603
37	20.4	61.8	360	28	BH496990
38	20.4	61.8	380	28	BH494004
39	20.4	61.8	399	28	BH743660
40	20.4	61.8	430	9	AI222038
41	20.4	61.8	509	28	BH682274
42	20.4	61.8	512	28	BH682764
43	20.4	61.8	536	28	BH497338
44	20.4	61.8	550	28	BH556094
45	20.4	61.8	557	28	BH508195

CM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 86.9596 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 cgggaattcaactacaacaccttggtttaaacgac 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	22.2	65.3	1323	10	AY208915	AY208915 Rattus no
c 2	22.2	65.3	1323	10	AY246699	AY246699 Mus muscu
c 3	22.2	65.3	1803	10	AF173380	AF173380 Mus muscu
c 4	22.2	65.3	3629	10	BC043321	BC043321 Mus muscu
c 5	22.2	65.3	5218	10	BC041777	BC041777 Mus muscu
c 6	22.2	65.3	5219	10	BC042206	BC042206 Mus muscu
c 7	22.2	65.3	194355	2	AC116511	AC116511 Mus muscu
c 8	22.2	65.3	270745	2	AC097544	AC097544 Rattus no
c 9	21.8	64.1	180366	9	AC036196	AC036196 Homo sapi
c 10	21.8	64.1	183015	2	AC140064	AC140064 Homo sapi
c 11	21.8	64.1	194996	9	AC103858	AC103858 Homo sapi
c 12	21.8	64.1	222710	2	EX470169	EX470169 Danio rer
c 13	21.6	63.5	246099	2	AC106365	AC106365 Rattus no
c 14	21.4	62.9	43469	3	CER07B7	275955 Caenorhabdi
c 15	21.4	62.9	111103	9	AC007129	AC007129 Homo sapi
c 16	21.4	62.9	122351	9	AC023157	AC023157 Homo sapi
c 17	21.4	62.9	130377	2	AC122130	AC122130 Homo sapi
c 18	21.4	62.9	148481	2	AC122139	AC122139 Homo sapi
c 19	21.4	62.9	189209	2	AC099649	AC099649 Homo sapi
c 20	21.4	62.9	192343	2	AC126596	AC126596 Mus muscu
c 21	21.4	62.9	195743	2	AC016774	AC016774 Homo sapi
c 22	21.4	62.9	203842	9	AC010789	AC010789 Homo sapi
c 23	21.4	62.9	228736	2	AC136565	AC136565 Rattus no
c 24	21.4	62.9	262820	2	AC137354	AC137354 Rattus no
c 25	21.4	62.9	263406	2	AC129276	AC129276 Rattus no
c 26	21.4	62.9	267768	2	AC133021	AC133021 Rattus no
c 27	21.4	62.9	271639	2	AC137481	AC137481 Rattus no
c 28	21.2	62.4	272	11	G70578	G70578 VEO024311FB
c 29	21.2	62.4	291	11	G71357	G71357 VEO024311FB
c 30	21.2	62.4	300	11	G71180	G71180 VEO182311FB
c 31	21.2	62.4	328	11	G70613	G70613 VEO182311FB
c 32	21.2	62.4	172358	2	AC120612	AC120612 Rattus no
c 33	21	61.8	172193	2	AC113567	AC113567 Canis fam

c 34 21 61.8 177015 9 AC108137
c 35 21 61.8 224735 2 AC132661
c 36 21 61.8 227693 2 AC095313
c 37 21 61.8 233886 2 AC128261
c 38 21 61.8 244042 2 AC103004
c 39 21 61.8 290791 2 AC137023
c 40 21 61.8 305488 2 AC111881
c 41 20.8 61.2 659 11 G73168
c 42 20.8 61.2 4773 14 PPV6GP
c 43 20.8 61.2 40133 9 AC073331
c 44 20.8 61.2 40328 9 HSAC000021
c 45 20.8 61.2 43795 9 AC000022

Search completed: October 21, 2003, 17:18:16
Job time : 90.9596 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:18 ; Search time 6.5374 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 cggaaattactacaacatttcgtttaagcgc 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*

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9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*

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13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	100.0	34	21	Mouse A1IP gene pr
c 2	22.2	65.3	1323	21	Mouse A1IP coding
c 3	22.2	65.3	1803	21	Mouse A1IP gene.
c 4	21.4	62.9	32169	22	Human nervous syst
c 5	21.4	62.9	32169	22	Human nervous syst
c 6	21.4	62.9	32169	23	Human testicular a
c 7	21.4	62.9	32189	22	Human nervous syst
c 8	21.4	62.9	32189	22	Human reproductive
c 9	21.4	62.9	32189	23	Human testicular a
c 10	21.4	62.9	33971	22	Human immune/haema
c 11	21.2	62.4	287	24	Corn tassal-deriva
c 12	21	61.8	354	21	Mouse A1IP coding
c 13	20.8	61.2	40328	21	Human DAZ genomic
c 14	20.8	61.2	43795	21	Human DAZ genomic
c 15	20.4	60.0	1463	24	Pasteurella haemol
c 16	20.2	59.4	262	21	Rat hepatocyte car
c 17	20.2	59.4	1026	20	Human secreted pro
c 18	19.8	58.2	252	25	Human GDP-mannose
c 19	19.8	58.2	288	25	Human GDP-mannose
c 20	19.8	58.2	387	22	Human polynucleoti
c 21	19.8	58.2	2176	22	Human cDNA sequenc
c 22	19.6	57.6	583	24	Arabidopsis thalia
c 23	19.6	57.6	820	25	Human colon specif
c 24	19.6	57.6	839	25	Human colon specif
c 25	19.6	57.6	8078	22	Tumour suppressor
c 26	19.4	57.1	348	23	Human prostate exp
c 27	19.4	57.1	349	23	Human prostate exp
c 28	19.4	57.1	400	23	Human prostate exp
c 29	19.4	57.1	418	23	Human prostate exp
c 30	19.4	57.1	418	23	Human prostate exp
c 31	19.4	57.1	465	23	Human prostate exp
c 32	19.4	57.1	465	23	Human prostate exp
c 33	19.4	57.1	465	23	Human prostate exp
c 34	19.4	57.1	607	24	Oligonucleotide fo
c 35	19.4	57.1	607	24	Oligonucleotide fo
c 36	19.4	57.1	800	23	Human prostate exp
c 37	19.4	57.1	801	23	Human prostate exp
c 38	19.4	57.1	801	23	Human prostate exp
c 39	19.4	57.1	801	23	Human prostate exp
c 40	19.4	57.1	801	23	Human prostate exp
c 41	19.4	57.1	801	23	Human prostate exp
c 42	19.4	57.1	1519	22	Arabidopsis thalia
c 43	19.4	57.1	2948	23	Arabidopsis thalia
c 44	19.4	57.1	8934	23	Drosophila melanog
c 45	19.2	56.5	452	21	N. meningitidis pa

ALIGNMENTS

RESULT 1
 AAZ99095
 ID AAZ99095 standard; DNA; 34 BP.
 XX
 AC AAZ99095;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE Mouse ATIP gene primer oligo.antisens.
 XX
 KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
 KW two-hybrid screen; signal transduction; PCR primer.
 XX
 OS Mus sp.
 XX
 FN FR2782084-A1.
 XX
 PD 11-FEB-2000.
 XX
 PF 04-AUG-1998; 98FR-0009997.
 XX
 PR 04-AUG-1998; 98FR-0009997.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Elbaz N, Nahmias C, Strosberg AD;
 XX
 DR WPI; 2000-248410/22.
 XX
 XX Nucleic acids coding for angiotensin II receptor AT2 interacting
 PT proteins useful in screening assays for receptor-protein interaction -
 XX
 PS Claim 4; Page 16; 63pp; French.
 XX
 CC Primers AAZ99094-299095 were used to PCR amplify the cDNA encoding a
 CC mouse angiotensin II (AT2) receptor interactive protein (ATIP; AA83777).
 CC The initial clone (AAZ99090) was isolated from a two-hybrid screen using
 CC the C-terminal fragment of the mouse AT2 receptor as the "bait"
 CC (AA83781). The "target" is a mouse foetal cDNA library. Cells
 CC transformed with vectors containing the cDNA, or immobilized proteins
 CC encoded by it, can be used to screen for substances that modulate
 CC ATIP-AT2 interaction or substances that interact with ATIP, especially
 CC using yeast two- or three-hybrid techniques. Such substances may be
 CC useful for treating disorders associated with anomalous AT2 receptor
 CC signal transduction.
 XX
 SQ Sequence 34 BP; 10 A; 10 C; 4 G; 10 T; 0 other;
 Query Match 100.0%; Score 34; DB 21; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGGAATTCACACACCTTCGTTTAAGCATC 34
 Db 1 CCGGAATTCACACACCTTCGTTTAAGCATC 34

c	1	21.4	62.9	32169	11	US-09-764-891-8605	Sequence 8605, Ap
c	2	21.4	62.9	32189	11	US-09-764-891-8604	Sequence 8604, Ap
c	3	21.2	62.4	254	9	US-09-923-876-1426	Sequence 1426, Ap
c	4	21.2	62.4	287	9	US-09-294-093B-4203	Sequence 4203, Ap
c	5	21	61.8	325	11	US-09-535-459-1205	Sequence 1205, Ap
c	6	20.2	59.4	1026	11	US-09-974-879-36	Sequence 36, Appl
c	7	20.2	59.4	1026	11	US-09-305-736-36	Sequence 36, Appl
c	8	19.8	58.2	252	10	US-09-878-574-10612	Sequence 10612, A
c	9	19.8	58.2	288	10	US-09-878-574-8275	Sequence 8275, Ap
c	10	19.8	58.2	875	13	US-10-627-632-121215	Sequence 121215, A
c	11	19.8	58.2	1572	11	US-09-918-624B-31	Sequence 31, Appl
c	12	19.6	57.6	583	10	US-09-938-842A-5265	Sequence 5265, Ap
c	13	19.6	57.6	729	13	US-10-027-632-111429	Sequence 111429, A
c	14	19.6	57.6	820	13	US-10-016-634A-26	Sequence 26, Appl
c	15	19.6	57.6	839	13	US-10-016-634A-27	Sequence 27, Appl
c	16	19.4	57.1	292	12	US-10-006-285-147	Sequence 147, App
c	17	19.4	57.1	504	12	US-10-006-285-339	Sequence 339, App
c	18	19.2	56.5	19972	12	US-10-311-455-79	Sequence 79, Appl
c	19	19.2	56.5	62804	13	US-10-096-960-3	Sequence 3, Appli
c	20	19	55.9	554	9	US-09-864-761-12250	Sequence 12250, A
c	21	19	55.9	624	13	US-10-027-632-248142	Sequence 248142, A
c	22	19	55.9	630	12	US-10-032-585-6392	Sequence 6392, Ap
c	23	19	55.9	77992	12	US-10-225-810-11	Sequence 11, Appl
c	24	19	55.9	250000	12	US-10-225-810-26	Sequence 26, Appl
c	25	19	55.9	322101	12	US-10-060-902-1	Sequence 1, Appli
c	26	18.8	55.3	438	13	US-10-027-632-74900	Sequence 74900, A
c	27	18.8	55.3	438	13	US-10-027-632-299653	Sequence 299653, A
c	28	18.8	55.3	736	13	US-10-027-632-144102	Sequence 144102, A
c	29	18.8	55.3	3655	13	US-10-027-632-259680	Sequence 259680, A
c	30	18.8	55.3	715517	13	US-10-027-632-53712	Sequence 53712, A
c	31	18.6	54.7	444	10	US-09-938-842A-412	Sequence 412, App
c	32	18.6	54.7	593	13	US-10-027-632-96754	Sequence 96754, A
c	33	18.6	54.7	593	13	US-10-027-632-306323	Sequence 306323, A
c	34	18.6	54.7	669	9	US-09-770-149-424	Sequence 424, App
c	35	18.6	54.7	1630	14	US-10-084-817-201	Sequence 201, App
c	36	18.6	54.7	2940917	13	US-10-027-632-174763	Sequence 174763, A
c	37	18.4	54.1	506	13	US-10-027-632-79342	Sequence 79342, A
c	38	18.4	54.1	506	13	US-10-027-632-301157	Sequence 301157, A
c	39	18.4	54.1	636	13	US-10-027-632-214275	Sequence 214275, A
c	40	18.4	54.1	710	13	US-10-027-632-151884	Sequence 151884, A
c	41	18.4	54.1	1126	13	US-10-027-632-249133	Sequence 249133, A
c	42	18.4	54.1	1126	13	US-10-027-632-249134	Sequence 249134, A
c	43	18.4	54.1	2470	13	US-10-027-632-260176	Sequence 260176, A
c	44	18.4	54.1	2747	9	US-09-778-927A-24	Sequence 24, Appl
c	45	18.4	54.1	1830121	14	US-10-329-960-1	Sequence 1, Appli

Search completed: October 22, 2003, 04:13:49
Job time : 28.9566 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 6.95661 Seconds
(without alignments)
13107.130 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 cgggaattactacaacatttcgtttaagcgc 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues
Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
No.						

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 53.6043 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 ccggaattactacaacatttcgtttaagcgc 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estha:
2: em_esthum:
3: em_estin:
4: em_estm:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_htc:
9: gb_estl:
10: gb_est2:
11: gb_htc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_man:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rod:
26: em_gss_phg:
27: em_gss_vrl:

28: gb_gssl:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	22.8	67.1	276	9	AV296549
2	22.8	67.1	516	12	BW261570 dat160211
3	22.4	65.9	508	12	B3056698 BJ056698
4	22.4	65.9	628	10	BG022525 da005a09
5	22.4	65.9	642	9	AW767695 da77f06.x
c 6	22.2	65.3	450	14	CA556858 K0218E03
c 7	22.2	65.3	509	12	BI319660
c 8	22.2	65.3	517	10	BE652532
c 9	22.2	65.3	541	4	BX512030 RZPD Mus
c 10	22.2	65.3	600	13	B0921755
c 11	22.2	65.3	657	10	BB628131
c 12	22.2	65.3	667	14	BY742653
c 13	22.2	65.3	734	14	CB316595 AGENCOURT
c 14	22.2	65.3	748	10	BF141309 601789830
c 15	22.2	65.3	920	13	BU523654 AGENCOURT
c 16	22.2	65.3	950	13	BQ921402
17	22.2	65.3	1090	29	CC220629
c 18	22.2	65.3	2477	11	AK030510 Mus muscu
c 19	22.2	65.3	3237	11	AK035576 Mus muscu
c 20	22.2	65.3	3963	11	AK031693 Mus muscu
21	21.8	64.1	271	9	AI920645
22	21.8	64.1	600	14	CA659570 wml.pK00
23	21.6	63.5	812	28	BH397605 AG-ND-133
c 24	21.4	62.9	1125	12	BK464322 AGENCOURT
25	21.2	62.4	263	9	AI947351
26	21.2	62.4	325	10	BG349168 947028F09
27	21.2	62.4	358	9	AW120381 614060A08
28	21.2	62.4	369	9	AW017677 614061G01
c 29	21.2	62.4	385	9	AW056048 660002A05
c 30	21.2	62.4	418	9	AW063792
31	21.2	62.4	454	9	AI629809 486039D07
c 32	21.2	62.4	527	28	BH107504 RPOC-24-3
33	21.2	62.4	544	13	BQ668252 946134D05
34	21.2	62.4	545	13	BQ703374 946138H11
35	21.2	62.4	549	9	AI737756 605040H03
c 36	21.2	62.4	554	9	AW067499 660013C08
37	21.2	62.4	564	12	BK378462 MES1564-D
38	21.2	62.4	571	14	CD527810 3529.1.12
39	21.2	62.4	573	10	BE344835 946029D01
40	21.2	62.4	580	9	AW126505 614101E06
c 41	21.2	62.4	582	9	AW042241 614024501
42	21.2	62.4	590	14	CA398895 EL0140311
43	21.2	62.4	591	9	AI622281 486034D07
44	21.2	62.4	592	28	AQ423423 CIT31-EI-
45	21.2	62.4	604	9	AI491677 486024F02

Search completed: October 21, 2003, 21:04:27
Job time : 56.6043 secs